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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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      9n:
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seq length: 2000000000
         protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
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      BLOSUM62
Gapop 10.0 , Gapext 0.5
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59
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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                    US-08-799-173A-8
US-07-862-021B-15
PCT-US93-03164-15
US-08-2417-495-26
US-08-218-950-26
US-09-218-950-26
PCT-US92-01785-26
PCT-US92-01785-26
PCT-US93-03164-12
US-07-862-021B-14
PCT-US93-03164-12
US-08-313-288B-12
PCT-US93-03164-12
US-08-313-288B-12
US-08-313-288B-10
US-08-313-338B-10
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Sequence
Patent No.
Sequence
                                                                Sequence 8, Appli Sequence 15, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appli Sequence 7, Appli Sequence 14, Appl Sequence 14, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 14, Appl Sequence 17, Appl Sequence 57, Appl Sequence 57
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                       4, Appli
4, Appli
1, Appli
57, Appli
57, Appl
57, Appl
57, Appl
57, Appl
51, Appli
1, Appli
51, Appli
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47 CMGPGC

Qy 15 CXGPGC 20	Query Match 61.0%; Score 36; DB 2; Length 52 Best Local Similarity 83.3%; Pred. No. 16; Matches 5; Conservative 0; Mismatches 1; Indels	US-08-799-173A-8 US-08-799-173A-8 Sequence 8, Application US/08799173A Patent NO. 5871969 GENERAL INFORMATION: DILLON TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR- NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STATE: MD COUNTRY: USA ZIP: 20850 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTION Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/799,173A FILING DATE: 11-FEB-1997 CLASSIFICATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 9526 ATTORNEY/AGENT INFORMATION: NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 9F226 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8512 INFORMATION FOR SED ID NO: 8: SEQUENCE CHARACTERISTICS: LEMGTH: 52 amino acids TYPE: protein US-08-799-173A-8	ALIGNMENTS	28 31 52.5 992 1 US-08-482-847-1 29 31 52.5 1063 1 US-08-093-453B-3 30 31 52.5 1063 1 US-08-127-499A-8 31 31 52.5 1063 1 US-08-127-499A-8 32 31 52.5 1214 2 US-08-231-193A-54 33 31 52.5 1214 2 US-08-486-273A-54 34 31 52.5 1214 3 US-08-440-0474-54 35 31 52.5 1214 3 US-08-940-086A-54 36 31 52.5 1219 2 US-08-231-193A-50 37 31 52.5 1219 2 US-08-231-193A-50 38 31 52.5 1219 2 US-08-486-273A-50 39 31 52.5 1219 3 US-08-486-273A-50 40 31 52.5 1219 3 US-08-231-193A-48 41 31 52.5 1231 2 US-08-231-193A-48 42 31 52.5 1231 3 US-08-240-086A-48 43 31 52.5 1231 3 US-08-480-474-48 43 31 52.5 1231 3 US-08-480-474-8 44 31 52.5 1231 3 US-08-940-086A-48 45 31 52.5 1236 2 US-08-231-193A-6
	52; ls 0;	μ		sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence
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RESULT 2 US-07-862-021B-15

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CPCT-US93-03164-15; Sequence 15, Applicat; GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Jessell, The
APPLICANT: Klar, Avihu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                               ADDRESSEE: Cooper & Dunham
                                                                                                                                                                              APPLICANT: Jessell, Thomas M
APPLICANT: Klar, Avihu
APPLICANT: Klar, Avihu
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                      ZIP:
                                                                                                                                                                                                                                                                                                                                                   49 CMGPGC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 59 amino TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                   15 CXGPGC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                      10112
                                                                                                  New York
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New York
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                                                                                                                  30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 Rockefeller Plaza
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/08417495 Patent No. 5843728
FILING DATE:
APPLICATION UMBER: 07/665,961
FILING DATE: March 7, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/119002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,495
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seed, Br
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAN: (212) 664-0525
TELEEX: 422523 COOP UI
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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STREET: 2.
STREET: 4A
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
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CLASSIFICATION:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish .... Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                       APPLICATION NUMBER: US/07/847,566
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AMINO ACID
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VENTION: Redirection of Cellular Immunity by
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27
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83.3%;
                                                                                                                                                                            US/08/203,866
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Pred. No.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

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Best Local Similarity 83...
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 Patent No.
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/2.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-04200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 542-09U
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: (220 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 176 FOR CITY: BOSTON STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 02-AUG-1994 CLASSIFICATION: 514
                STRANDEDNESS: sir
TOPOLOGY: linear
                                                 LENGTH: * 220 amino acids
TYPE: amino acid
                                                                                                                                          TELEPHONE: 617-428-02
TELEFAX: 617-428-7045
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176 Federal Street
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Pred. No.
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21 CLGPGC 15 CXGPGC 20

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Conservative

Mismatches

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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-09-218-950-26
Query Match
Best Local Similarity
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Best Local Similarity 83...
Matches 5; Conservative
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Seed, J
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110
COMPUTER READABLE FORM:
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ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROMEO, Charles
APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
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OPERATING SYSTEM:
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CITY: Boston
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Romeo, Charles
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                              61.0%;
83.3%;
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                              Score 36; DB
Pred. No. 48;
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Pred. No. 48;
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PCT-US95-00454-26; Sequence 26, Application PC/TUS9500454; GENERAL INFORMATION:
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Best Local Similarity
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CLASSIFICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/665,961
FILING DATE: MARCH 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
NAME: Clark, Paul T.
07/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application PC/TUS9201785
GENERAL INFORMATION:
APPLICANT: The General Hospital Co
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CURRENT APPLICATION DATA:
APPLICATION NATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                          APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Targeted Cytolysis of HIV-Infected
TITLE OF INVENTION: Cells by Chimeric CD4 Receptor-
TITLE OF INVENTION: Bearing Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor
TITLE OF INVENTION: Chimeras
                                                                                                                                   CORRESPONDENCE ADDRESS
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ADDRESSEE: Fish & Richardson
                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                     ADDRESSEE:
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                                   02110-2804
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AMINO ACID
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225 Franklin Street
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83.3%;
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7, 1991
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Pred. No.
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; MOLECULE TYPE: amino acids
PCT-US95-00454-26
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Best Local
                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 11-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847
FILING DATE: March 6, 1992
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OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HASTINGS, GREGG,
APPLICANT: PATRICK J. DILLON
TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                   NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: March CLASSIFICATION:
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CLASSIFICATION:
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                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 30,162
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9410 KEY WEST AVENUE
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March 7, 1991
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83.3%;
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Pred. No.
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INFORMATION FOR SEQ ID NO:

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TELECOMPUL.:

TELEPHONE: (2-64-C)

TELEX: (212) 664-C

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
"""E: AMINO ACID
"""DE: AMINO ACID
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-799-173A-7
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Best Local Similarity
""" Specification of the conserver of th
RESULT 11
PCT-US93-03164-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein
US-07-862-021B-14
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                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jessell, Thomas M APPLICANT: Klar, Avihu
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                                                                                                                                            248 CMGPGC 253
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FILING DATE: 19920405
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
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83.3%;
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Pred. No. 98;
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Pred. No. 74;
                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                              Length 568;
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                                                                                                                                                                                                                                                                                 Indels
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Query Match
Best Local Similarity
Themes 5; Conserve
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US-07-862-021B-12
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GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M
APPLICANT: Klar, Avihu
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SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acid
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NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
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FILING DATE: 19930402
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                COUNTRY: U
ZIP: 10112
                                                                                                                                                                                                                                    CITY: New York
STATE: New York
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TELEX: 422523 COOP UI
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STATE: New York
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30 Rockefeller Plaza
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Pred. No. 98;
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; MOLECULE TYPE: US-08-313-288B-12
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US-08-313-288B-12
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Matches 5; Conserv
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
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                                                                                                 INFORMATION FOR SEQ ID NO:
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NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028
TELECOMMUNICATION INFORMATION:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acid
                                                                                                                                                          NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                TELEFAX: (212)
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                               TOPOLOGY:
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New York
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                                                                                                                                 (212) 278-0400
12) 391-0526
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CLONING, EXPRESSION AND USES OF A
NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 977-9550
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83.3%;
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Pred. No. 1.3e+02
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-03164-12
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                                                                                             Sequence 10, Application US/07862021B Patent No. 5279966
                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
             APPLICANT: Jessell, Thomas M
APPLICANT: Klar, Avihu
TITLE OF INVENTION: CLORING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES:
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REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                             15 CXGPGC 20
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TELEX: 422523 COOP UI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: POFILING DATE: 19930402
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Pred. No. 1.3e+02;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: New YOOK
COTT: New YOOK
COUNTRY: USA
ZIT: 10112
COMPUTER READRABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: USA
COMPUTER READRABLE FORM:
MEDIUM TYPE: Floppy disk
COURTRY: USA
COMPUTER READRABLE FORM:
MEDIUM TYPE: Floppy disk
COURTRY: USA
COMPUTER READRABLE FORM:
CORRENT APPLICATION DATA:
CORRENT APPLICATION NUMBER: US/07/862.021B
FILING DATE: 19920405
COURTRY: USA
COUNTRY: USA
COUNTRY:
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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5: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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Gapop 10.0 , Gapext 0.5
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49.995 Million cell updates/sec
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and is derived by analysis of the total score distribution Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

Result Query Query Description No. Score Match Length DB ID Description 1 37 62.7 20 22 AAB76413 ErbB2 binding pept 2 37 62.7 161 20 AAY13498 Tissue cement prot 4 36 61.0 6 22 AAB76420 ErbB2 binding pept 5 36 61.0 16 22 AAB76381 ErbB2 binding pept 7 36 61.0 16 22 AAB76382 ErbB2 binding pept 8 36 61.0 16 22 AAB76383 ErbB2 binding pept 9 36 61.0 16 22 AAB76384 ErbB2 binding pept 10 36 61.0 16 22 AAB76385 ErbB2 binding pept 11 36 61.0 16 22 AAB76387 ErbB2 binding pept 11 36 61.0 16 22 AAB76387 ErbB2 binding pept 11 36 61.0 16 22 AAB76387 ErbB2 binding pept 12 AAB76386 ErbB2 binding pept 13 AAB76387 ErbB2 binding pept 14 AB76387 ErbB2 binding pept 15 AAB76387 ErbB2 binding pept 16 AB76387 ErbB2 binding pept 17 AAB76387 ErbB2 binding pept 18 AAB76387 ErbB2 binding pept

Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -

WPI; 2001-123048/13.

Dennis MS;

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binding	ErbB2 binding pept

ALIGNMENTS

RESULT

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AAB76413
                                                                                                                                                                                                    Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabbolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's Chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
                                                                                                                     30-JUN-2000; 2000WO-US18283
                                                                                                                                           11-JAN-2001.
                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                        ErbB2 binding peptide amino acid sequence SEQ ID 64.
                                                                                                                                                                                                                                                                             10-APR-2001
                                                                                                                                                                                                                                                                                                  AAB76413;
                                                                                                                                                                                                                                                                                                                    AAB76413 standard; Peptide;
                                                                             (GETH ) GENENTECH INC.
                                                                                                 02-JUL-1999;
                                                                                                                                                              WO200101748-A2
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                 99US-0142232.
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RESULT
AAY21843
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Best Local Similarity
Matches 5; Conser
                                                                                                                     Baughn
Sather
                                                                                                                                                                                                                                                                                                                                                                                             ulcerative colitis; atopic dermatitis; dermatomyositis; emphysema; diabetes mellitus; atrophic gastritis; glomerulonephritis; gout; trauma; Grave's Disease; hypereosinophilia; irritable bowel syndrome; infection; lupus erythematosus; multiple sclerosis; myasthenia gravis; inflammation; osteoarthritis; osteoporosis; panoreatitis; polymyositis; scleroderma; osteoarthritis; osteoporosis; panoreatitis; polymyositis; scleroderma;
            Human signal-peptide containing protein coding sequences used treat cancer and immune responses
                                                               WPI; 1999-430242/36
N-PSDB; AAX82078.
                                                                                                                                                                                                                                           22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Addison's disease; adult respiratory distress syndrome; allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitus; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal-peptide containing protein; SIGP; human; cancer; immune response; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY21843 standard; Protein; 161 AA.
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                                                                                                                                                                                                          31-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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| ctgpgc
                                                                                                                   SK,
                                                                                                                                                                        INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                arthritis; Sjogren's syndrome; autoimmune thyroditis
                                                                                                                 Corley NC,
Shah P;
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83.3%;
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Pred. No. 15;
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                                                                                                                                     Hillman JL,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue cement protein; TCP; blood-feeding; ectoparasite; pharmaceutical; vaccine; tissue bonding; surgical wound; skin grafting; immunogen; infection; arthropod parasite.
                                                                                                              Tissue cement proteins produced by blood-feeding related polynucleotides
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                            This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blood-feeding ectoparasites. The TCP, in a pharmaceutical composition, is useful for therapy, as a vaccine or vaccine component. The TCP itself is used to immunize an animal for production of such a vaccine. The TCPs are useful for bonding animal tissues. This may be temporary or permanent bonding and used in, e.g. repair of incised surgical wounds, lacerations, skin grafting, etc. The TCP can also be used as a protective immunogen in the control of diseases caused by infections transmitted by arthropod parasites. The tick TCPs provide a non-immunogenic tissue cement capable of bonding mammalian tissue with great strength. The hardening or elastic
                                                                                                                                                                                                                                       Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
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                                                                                                                                 This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76599 are examples of the ErbB2 binding ligands of the invention. Sequences of the ErbB2 binding ligands of the invention. Sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, isochaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat
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RESULT 1
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                                                                                                                                                                                                                                                   metabolic disorder; nutritional deficiency; Alzheimer's disease;
Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                                                                                                                                                                                                                        Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;
                                                                                                                                                                                                                                                                                                                                                        ErbB2 binding peptide amino acid sequence
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11-JAN-2001.

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RESULT 7
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Best Local
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cc bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides CC represented in AAB76350 - AAB76420 and AAB76432 - AAB764509 are examples CC of the ErbB2 binding ligands of the invention. Sequences CC AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in CC the isolation of the peptides of the invention. The peptides compete for CC binding ErbB2 with naturally occurring ligands, and may be used to treat CC disorders characterized by over expression of HER2/ErbB2 such as cancers, CC diseases of the nervous system, musculature and epithelia, e.g. nervous CC system damage resulting from trauma, surgery, strokes, ischaemia, CC infection, metabolic disorders, nutritional deficiency or toxic agents. CC In particular the synthetic peptide ligands may be used to treat CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, CC and neuropathy associated with diabetes.
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                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                          peptide amino acid sequence SEQ ID
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invention relates to non-naturally occurring peptide to the human erbB2 gene product ${\tt ErbB2}$ (also known as

ligands which

16;

116pp;

English.

WPI; 2001-123048/13.

02-JUL-1999;

99US-0142232

(GETH) GENENTECH INC

30-JUN-2000; 2000WO-US18283

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disorders characterized by over expression of HER2/ErbB2 such as cancers diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia,
                                                      This invention relates to non-naturally occurring peptide ligands which bind to the human erbb2 gene product Erbb2 (also known as HER2). Peptides represented in ABB76350 - ABB76420 and ABB76432 - ABB76590 are examples of the Erbb2 binding ligands of the invention. Sequences of the Erbb2 binding ligands of the invention sequences used in ABB76421 - AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding Erbb2 with naturally occurring ligands, and may be used to treat
                                                                                                                                                                                                                                                Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
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                                                                                                                                                                                                           Disclosure; Figure 16; 116pp; English.
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ErbB2 binding ligands of the invention. Sequences
21 - AAB76431 represent antibody Fc amino acid sequen
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                           This invention relates to non-naturally occurring peptide ligands which CC bind to the human exbB2 gene product ErbB2 (also known as HER2). Peptides CC represented in AAB76350 - AAB76402 and AAB76432 - AAB76509 are examples CC of the ErbB2 binding ligands of the invention. Sequences CC AB76421 - AAB76431 represent antibody Fc amino acid sequences used in CC the isolation of the peptides of the invention. The peptides compete for CC binding ErbB2 with naturally occurring ligands, and may be used to treat CC disorders characterized by over expression of HER2/ErbB2 such as cancers, CC diseases of the nervous system, musculature and epithelia, e.g. nervous cystem damage resulting from trauma, surgery, strokes, ischaemia, CC infection, metabolic disorders, nutritional deficiency or toxic agents. CC In particular the synthetic peptide ligands may be used to treat CC In particular the synthetic peptide ligands may be used to treat CC In commer's disease, Parkinson's disease, epilepsy, multiple sclerosis, CC Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease CC and neuropathy associated with diabetes.
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                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 16;
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Search completed: November 21, 2001, 15:46:04 Job time: 67 sec

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Database
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59
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description.
1	37	62.7	204	5	Q27392	Q27392 trypanosoma
ν	37	62.7	475	N	P71952	p71952 mycobacteri
ω	36	61.0	562	4	8MUN6	Q9num8 homo sapien
4	36	61.0	614	11	Q9WV00	Q9wv00 mus musculu
ر.	36	61.0	624	4	094862	094862 homo sapien.
6	36	61.0	656	4	Q9P0U4	Q9p0u4 homo sapien
7	36	61.0	656	4	Q9P2V7	Q9p2v7 homo sapien
80	36	61.0	802	13	Q9W770	Q9w770 gallus gall
9	36	61.0	803	13	042114	042114 brachydanio
10	36	61.0	807	4	Q9нсв6	Q9hcb6 homo sapien
11	36	61.0	807	6	Q9GLX9	Q9glx9 bos taurus
12	36	61.0	808	13	042113	042113 brachydanio
13	36	61.0	814	Ç	Q9VK82	Q9vk82 drosophila
14	36	61.0	831	ر.	017516	017516 caenorhabdi
15	36	61.0	991	4	015043	015043 homo sapien
16	36	61.0	1042	4	Q9H4G6	Q9h4g6 homo sapien
17	36	61.0	1249	10	023289	023289 arabidopsis
18	36	61.0	1631	4	9094606	Q9y6u6 homo sapien
19	35	59.3	1637	6	8ASX60	Q9xsv8 bos taurus

RESULT

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	59.3
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O10660 rubella vir	O10659 rubella vir	O10658 rubella vir	O10657 rubella vir	O10656 rubella vir	_	010654 rubella vir		O10652 rubella vir	010651 rubella vir	Q43388 arabidopsis	006580 mycobacteri	Q9ttv5 bos taurus	Q46024 corynebacte	Q9sxp5 nicotiana t	Q9dw77 rat cytomeg	Q9h192 homo sapien	Q9gzz7 homo sapien	Q99782 homo sapien	Q9if37 avian infec	Q9gze8 caenorhabdi	Q9h191 homo sapien	014583 homo sapien	Q56142 salmonella	068137 rhodobacter	075851 homo sapien

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Matches 5
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027392;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2001 (TrEMBLrel. 1
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InterPro; IPR000169; ...
InterPro; IPR000168; ...
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPALN.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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104 CSGPGC 109
                                                             15 CXGPGC 20
                                                                                                                               Similarity
5; Conserv
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                    21602 MW;
                                                                                                                                                                 62.7%;
83.3%;
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01,
16,
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129:135-141(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                               Score 37; DB Pred. No. 12; 0; Mismatches
                                                                                                                                  0;
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P71952
ID P71952
P71952;
AC P71952;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 105, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 14, Last annotation update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 51.7 KDA POTEIN CY441.24C.
GN RV2655C OR MTCY441.24C.
GN RV2655C OR MTCY441.24C.
OS Mycobacterium tuberculosis.
OC Actinomycetales; Corynebacterineae; Mycobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; 
                                                                                                                                                                                                                                                                                                                        29 NUMBER 10 NUMBER 11 NUM
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                                                                                                                                                                                 Query Match
Best Local
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HOMO sapiens (Human).
Homo sapiens (Human).
Charvota; Metazoa; Chordata;
Charvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-i -SIMILARITY: IN THE C-TERMINUS TO SACCHAROPOLYSPORA ER: HYPOTHETICAL 28.9 KDA PROTEIN IN XIS 5'REGION (ORF1). EMBL; Z80225; CAB02331.1; -.
Tuberculist; Rv2655c; -.
Hypothetical protein.
SEQUENCE 475 AA; 51718 MW; AC6CFF691E5E8FEB CRC64;
                                                                                                                                                                                                                                                                                                                        InterPro; IPR001965; -
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1
SEQUENCE 562 AA; 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AK002127; BAA92094.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo Hwagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y. Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Malioniya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ11265 FIS, CLONE PLACE1009158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=PLACENTA;
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397
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nes 5; Conserv
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CIGPGC
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402
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                                                                                                                                               Conservative
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Pred.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; | Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                            3BA79F8DEF9D3D9C
                                                                                                                                           Mismatches
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                                                                                                                                                                         36;
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Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...axawa K., Ono Y., Takiguchi S.,
Ishii S., Kawai Y., Saito <sup>K</sup>
Y., Nagahari K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
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23;
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RESULT
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Best Local
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01-MAY-1999 (TrEMBLrel. 10, C)
01-MAY-1999 (TrEMBLrel. 16, L)
01-MAR-2001 (TrEMBLrel. 16, L)
*TAA0762 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Q9WV00;
01-NOV-1999
01-NOV-1999
01-MAR-2001
    SMART; SM00209;
NON_TER 1
SEQUENCE 624 A
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SEQUENCE
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Mus musculus (Mouse).
Arvota; Metazoa; Chordata; Arria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEATH
DIO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        094862
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Proc. Natl. Acad. Sci. U.S.A. 96:7992-7997(1999).
EMBL; AJ238332; CAB48401.1; -.
                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                          DNA Res.
                                                                                                                                                                                                                                                                                                                                        Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Kotani H., Nomura N., Ohara O.; Rotani H., Nomura N., Ohara O.; Indicate the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=BRAIN; PubMed=9872452; MEDLINE=99087487; PubMed=9872452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIAA0762
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Izpisua-Belmonte J.C., Martinez-A C.;
                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DIO-1 is a gene involved in onset of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99324176; PubMed=10393935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                 for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                 Pro; IPR000884; PF00090; tsp_1
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                                                                                                                                                                                                                    AB018305;
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                                                                                                                                                                                                                    5:277-286(1998).
018305; BAA34482.1;
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                                                                                          tsp_1; 6.
; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614
67366
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Primates;
                 70557
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83.3%;
            MW;
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Last annotation updat
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Pred.
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                 40F2238D29024D03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F3E6B8970333AADA
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43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyajima N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka A.,
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Query Match Best Local S Matches 5

Similarity 83... 5; Conservative

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Mismatches

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Best Local S
Matches 5
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Q1-OCT-2000 (TrEMBLrel. 1
Q1-MAR-2001 (TrEMBLrel. 1
PROTEIN CONTAINING CXXC D
PCCX1 OR DKFZP434F174.
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01-OCT-2000
01-OCT-2000
01-MAR-2001
TISSUE-TESTIS; Wambutt R., Heubner D., Mewe Submitted (JAN-2000) to the EMBL; AB031069; BAA96307.1; EMBL; AL136862; CAB66796.1;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=20261296; PubMed=10799292;

Fujino T., Hasegawa M., Shibata S., Kishimoto T.,

"PCCX1, a novel DNA-binding protein with PHD finge
is regulated by proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00628; PHD; 1.
Pfam; PF00008; zf-CXXC; 1.
SMART; SM00249; PHD; 1.
SEQUENCE 656 AA; 75687 MW;
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Biochem.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mol. Cell. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shin Voo K., Carlone D.L., Jacobsen B.M., Flodin A., Skalnik "Cloning of a mammalian transcriptional activator that binds unmethylated CpG motifs and shares a CXXC domain with DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=20153771; PubMed=10688657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9P0U4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                          Gassenhuber J., Wiemann
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InterPro; IPR002857; -.
Pfam; PF00628; PHD; 1.
Pfam; PF02008; zf-CXXC; 1.
SMART; SM00249; PHD; 1.
SEQUENCE 656 AA; 75711 MW;
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01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9W770;
01-NOV-1999
01-NOV-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00090; tsp_1; 6. Pfam; PF02014; Reeler; 1. SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at the floor plate.";
Neuron 23:233-246(1999).
EMBL; AF149302; AAD41495.1;
InterPro; IPR000884; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99325518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99211385; PubMed-10197528;
Debby-Brafman A., Burstyn-Cohen T.,
"F-Spondin, expressed in somite regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klar A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burstyn-Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mediates inhibition of distinct somite domains to neural crest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "F-spondin is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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                                                                                                                                                                   484 CMGPGC
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5; Conser
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5; Conserv
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                                                                                                                                                                                                                                                   Conservative
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                                                               PRELIMINARY;
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T., Tzarfaty V., Frumkin A.,
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90509
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                    61.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.0%;
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0; Mismatches
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    Last sequence update)
                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB
Pred. No. 45;
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                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                         0644D2BDD0A0FE12 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T., Klar A., Kalcheim C.; regions avoided by neural crest cells,
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Best Loc
Matches
                                                                                       Q9GLX9 PRELIMINARY;
Q9GLX9;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, I
01-MAR-2001 (TrEMBLrel. 16, I
VSGP/F-SPONDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (Tr
01-MAR-2001 (Tr
01-MAR-2001 (Tr
VSGP/F-SPONDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoting factor from bovine ovarian follicular cloning from bovine and human ovary."; Cloning from bovine and human ovary."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ daEMBL; AB051390; BAB18461.1; -. SEQUENCE 807 AA; 90987 MW; 06FC52484206BB55
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                  Bos taurus (Bovine).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyamoto K., Morishita Y., Yamazaki M., Minamino N., Kangawa
Matsuo H., Mizutani T., Yamada K., Minegishi T.;
"Isolation and characterization of vascular smooth muscle ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Miyamoto K., Moris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9НСВ6
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PF02014; Reeler; 1.
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NCE 803 AA; 90331 MW;
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Primates;
Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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83.3%;
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83
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16,
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Pred. No.
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     Ruminantia; Pecora; Bovoidea;
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; Ostariophysi;
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01-JAN-1998
01-JAN-1998
01-MAR-2001
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
                                                                                                                                                                                                                               SMART; SM
SEQUENCE
                                                                    Q9VK82;
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoting factor from bovine ovarian follicular cloning from bovine and human ovary."; submitted (NOV-2000) to the EMBL/GenBank/DDBJ da EMBL; AB051389; BAB18460.1; -. SEQUENCE 807 AA; 90976 MW; 4C484B331FB1034C
                                            Drosophila
                                                    CG6417 PROTEIN. CG6417.
                                                                                                                                                                                                                                       Pfam; PF00090; tsp_1; 6.
Pfam; PF02014; Reeler; 1.
SMART; SM00209; TSP1; 1.
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Dev. Biol. 0:0-0(1997).
EMBL; AB006086; BAA22810.1;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Rasborinae; C
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Matsuo H., Mizutani T., Yamada K., Minegishi T.;
"Isolation and characterization of vascular smooth muscle cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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InterPro; IPR002861; -.
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NCBI_TaxID=9913;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue R C. Siden Kismos I. Simner M. Styneki M. D. Smith T.
                                                                                                                                                                                                                                     017516 PRELIMINARY:
017516;
01-JAN-1998 (TIEMBLIEL:
01-JAN-1998 (TIEMBLIEL:
01-NOV-1998 (TIEMBLIEL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X. Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A. Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng Glübs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                          STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                   SEQUENCE FROM N.A.
                                                                                                        Eukaryota; Metazoa; Nematu
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                        Caenorhabditis elegans
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Pred. No.
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O15043;
O1-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-MAR-2001 (TrEMBLrel. 1
                                                                                                                                                            "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain wicode for large proteins in vitro.";
DNA Res. 4:141-150(1997).
EMBL; ABOO2331; BAA207931.1; -.
InterPro; IPR001052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson & Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
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SEQUENCE
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Homo sapiens (Human).
Homo sapiens (Human).
'-rvota; Metazoa; Chordata; '-rvota; Primates;
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Bradshaw H., Devlin |
Submitted (JUL-1997)
                                                                                       SMART;
                                                                                                 PRINTS; PR00163; RUBREDOXIN.
PROSITE; PS00527; RIBOSOMAL_
                                                                                                                           Pfam; PF00628; PHD;
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InterPro; IPR001209; -.
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                                                                                     SM00249; PHD;
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در:
در:
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            61.0%;
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16,
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                                                              MW;
Score 36; DB Pred. No. 63; 0; Mismatches
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A; Dicture: France: DNA
A; Molecule type: DNA
A; Residues: 1-220 < KAS>
A; Residues: 1-220 < KAS>
A; Cross-references: GB: M31773; NID: g199032; PIDN: AAA39494.1; PID: g387413
A; Cross-references: GB: M31773; NID: g199032; PIDN: AAA39494.1; PID: g387413 mb-1 protein precursor - mouse
N;Alternate names: surface IgM complex alpha chain
C;Species: Mus musculus (house mouse)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 05-Nov-1999
C;Accession: A43540; S01648; A60228; A39398; I57521
R;Kashiwamura, S. I.; Koyama, T.; Matsuo, T.; Steinmetz, M.; Kimoto, M.; Sakaguchi, N.
J. Immunol. 145, 337-343, 1990
A;Title: Structure of the murine mb-1 gene encoding a putative sIgM-associated molecu
A;Reference number: A43540; MUID:90293481
A;Accession: A43540 В Qy A,cross-reterences: GB:280225; GB:AL123456; NID:g3242265; PIDN:CAB02331.1; PID:e26652 A;Experimental source: strain H37Rv C;Genetics: A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-475 <COL> Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete hypothetical protein Rv2655c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: C70966
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, IR; Cole, S.T.; Brosch, R.; Parkhill, R.; Cole, S.T.; Brosch, R.; Parkhill, R.; Cole, S.T.; Churcher, C.; Harris, R.; Cole, S.; A43540 A; Gene: A; Reference number: A70500; MUID: 98295987 A; Accession: C70966 A;Status: preliminary Query Match Best Local S Matches 5 ;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; 439 CSGPGC 444 15 CXGPGC 20 Rv2655c lymphocyte lineage-restricted e number: S01648; MUID:89091088 . Similarity 5; Conserv Conservative 62.7%; 83.3%; 0; Score 37; Pred. No. Mismatches expression of mb-1, a gene with CD3-like DB 2; Length 475; Indels C.; Harris, D.; Hamlin, 0; Gaps Z .. .; Gordon Holroyd, 0: geno

structural structural

structural

polypro polypro polypro

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RESULT 3
A47723
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos i A;Reference number: A47723; MUID:93376785
                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-803 <RUI>
A;Cross-references: GB:L09123; NID:g409244; PIDN:AAA19105.1; PID:g409245
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>
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Bur. J. Immunol. 20, 2795-2799, 1990
A;Title: Identification of the genes encoding the IgM-alpha A;Referrence number: A60228; MUID:91099432
A;Accession: A60228
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F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-220/Product: mb-1 protein #status predicted <MAT>
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A;Residues: 'X',30-38 <CAM>
R;Travis, A.; Hagman, J.; Grosschedl,
Mol. Cell. Biol. 11, 5756-5766, 1991
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A; Residues: 29-38 < NOM:
R; Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
R; Campbell, K.S.; Hager, B.B.; 3982-3986, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
A; Title: IgM antigen receptor complex contains phosphoprotein products
A; Reference number: A39398; MUID:91219496
A; Accession: A39398
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A;Residues: 1-220 <SAK>
A;Cross-references: EMBL:X13450; NID:g53015; PIDN:CAA31801.1; PID:g53016
R:Hombach, J.; Lottspeich, F.; Reth, M.
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A; Residues: 1-15, 'QA' <RES>
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A; Molecule type:
A; Residues: 1-220
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RESULT
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A; Molecule type: mRNA
A; Residues: 1-807 < KLA>
A; Residues: 1-807 < KLA>
A; Residues: 1-807 < KLA>
A; Cross-references: GB: M88469; NID: 9204176; PIDN: AAA41174.1; PID: 9204177
A; Experimental source: embryo floor plate
A; Experimental source: embryo floor plate
C; Superfamily: F-spondin; thrombospondin type 1 repeat homology < THR2>
F; 441-495/Domain: thrombospondin type 1 repeat homology < THR3>
F; 503-665/Domain: thrombospondin type 1 repeat homology < THR4>
F; 613-666/Domain: thrombospondin type 1 repeat homology < THR5>
F; 667-721/Domain: thrombospondin type 1 repeat homology < THR5>
F; 677-721/Domain: thrombospondin type 1 repeat homology < THR5>
F; 677-721/Domain: thrombospondin type 1 repeat homology < THR6>
C:Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C:Accession: H71404
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, July 1997 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein ZC132.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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T15108
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Cell 69, 95-110, 1992
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C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A38152
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:ZC132.4
A;Map position: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF014939; NID:g2275620; PID:g2275624; PIDN:AAB63927.1; GSPDB
A;Experimental source: strain Bristol N2; clone 2C132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-831 <BRA>
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R;Bradshaw, H.;
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                                                                                                           hypothetical protein d13195c - Arabidopsis thaliana
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nes 5; Conserv
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C.; Bergkamp,
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Giel B.

C; Function:

64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1 C; Complex: Laminins are trimers of an alpha-

Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type

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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1786 < VUO>
A; Residues: 1-1786 < VUO
A; Residues: 1-178
A;Cross-references: GDB:119357; OMIM:150240
A;Map position: 7q31.1-7q31.3
A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3;
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A;Residues: 1-1786 <PRIX>
A;Residues: 1-1786 <PRIX>
A;Cross-references: GB:M61951; GB:J02778; NID:g186911; PIDN:AAA59486.1; PID:g186913
A;Cross-references: GB:M61951; GB:J02778; NID:g186911; PIDN:AAA59486.1; PID:g186913
A;Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.
Am. J. Hum. Genet. 41, 605-615, 1987
A;Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localizat A;Reference number: A26994; MUID:88021029
A;Accession: A26994; MUID:88021029
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N;Alternate names: laminin chain B1
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001
C;Accession: S13547; A28483; A26994; S23566
R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 15611-15616, 1990
A;Title: Structure of the human laminin B1 chain gene.
A;Reference number: S13547; MUID:90368768
A;Accession: S13547
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J. Biol. Chem. 262, 10454-10462, 1987
A;Title: Human laminin B1 chain. A mu
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C; Superfamily: Arabidopsis thaliana hypothetical protein d13195c
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A; Residues: 1-1249 <BEV>
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                                                                                                                                                                                                                            C; Genetics:
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A; Residues: 762-1786 < VU2>
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                                                                                                                                                                                                                                                                           A; Note: mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 CGGPGC 17
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83.3%;
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Benes, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                en, T.; Tryggvason,
pp. 175-193, Acader
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Rechman, S.; Ans
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A;Molecule type: mRNA
A;Residues: 1-1786 <SAS>
A;Cross-references: EMBL:M15525; NID:g198700
A;Cross-references: EMBL:M15525; NID:g198700
A;Note: translation in GenBank has additional 48 residues
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.;
Blochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosacch
A;Reference number: S02678; MUID:88326259
A;Accession: S02679
                                                                                                                                                                                                                                                                                                                                                     laminin beta-1 chain precursor - mouse
N;Alternate names: laminin chain B1
C;Species: Mus musculus (house mouse)
C;Date: 28:Feb-1986 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543
R;Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.
Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987
A;Title: Sequence of the CDNA encoding the laminin B1 chain reveals a multic A;Reference number: A26413; MUID:87147212
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F;1084-1129/Domain: laminin-type EGF-like homology <LEI1>
F;1132-1176/Jomain: laminin-type EGF-like homology <LEI1>
F;1131-139/Domain: I <LODM2>
F;1179-1397/Region: heptad repeats
F;1398-1430/Jomain: alpha <ALP>
F;1431-1786/Jomain: I <LODM1>
F;1431-1786/Jomain: I <LODM1>
F;1431-1786/Jomain: alpha <ALP>
F;1431-1786/Region: heptad repeats
F;1431-1786/Region: heptad repeats
F;120,356,7519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding :
A; Molecule type: protein A; Residues: 28-42; 932-946 R; Hartl, L.; Oberbaeumer, Eur. J. Biochem. 173, 629-
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F;510-540/Domain: laminin-type EGF-like
F;549-774/Domain: IV <DOM4>
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F;271-548/Domain: V <DOM5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1179,1182,1785/Disulfide bonds: interchain #status predicted
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F;335-395/Domain:
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     L.; Oberbaeumer, I.; Biochem. 173, 629-635,
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5; Conserv
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                                                          <FUJ>
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Pred. No. 1.1e+02;
0; Mismatches 1;
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F:335-395/Domain: laminin-type
F;398-455/Domain: laminin-type
F:458-507/Domain: laminin-type
F:510-540/Domain: laminin-type
F:541-772/Domain: IV COOM4>
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Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments
A;Reference number: S01790; MUID:89030693
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A; Molecule type: mRNA
A; Residues: 1292-1530, 'MEMP', 1535-1691, 'C', 1693-1748, 'N', 1750-1786 CBAR>
A; Cross-references: EMBL:X05212; NID:g52861; PIDN:CAA28839.1; PID:g809042
A; Cross-references: EMBL:X05212; NID:g52861; PIDN:CAA28839.1; PID:g809042
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
                                                                                                                                                                                                                                               F;1028-1081/Domain: laminin-type EGF-like F;1084-1129/Domain: laminin-type EGF-like F;1133-1176/Domain: laminin-type EGF-like
                                                                                                                                                                                                                                                                                                                                                                                   F;773-1182/Domain: III <POM3>
F;773-918/Domain: laminin-type EGF-like
F;821-864/Domain: laminin-type EGF-like
F;867-914/Domain: laminin-type EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: interact with cells and with other basement membrane proteins C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C;Keywords: basement membrane; calcium binding; cell binding; coiled toil; ex
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R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo,
EMBO J. 4, 309-316, 1985
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Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments
A;Reference number: S08895; MUID:89078415
A;Accession: S14877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1-21/Domain: signal sequence #status predicted <SIG>F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>
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A; Residues: 1700-1748,'N', 1750-1759 <PAU:
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A: Residues: 1561-1587 < DEU>
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R;Mann, K.;
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A: Residues: 457-466; 854-868; 932-946 < HAR>
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                                                                                                                   F;1431-1786/Domain:
                                                                                                                                                                         F;1398-1430/Domain:
                                                                                                                                                                                            F;1183-1397/Region: heptad repeats
                                                                                                                                                                                                                              F;1183-1397/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;271-332/Domain: laminin-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A02871
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                                                                                                                                                                                                                                                                                                                              ;773-818/Domain: laminin-type EGF-like homology <LE06>;821-864/Domain: laminin-type EGF-like homology <LE07>;867-914/Domain: laminin-type EGF-like homology <LE08>;917-973/Domain: laminin-type EGF-like homology <LE09>;917-973/Domain: laminin-type EGF-like homology <LE10>;976-1025/Domain: laminin-type EGF-like homology <LE10>
22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) :30-35/Disulfide bonds: #status predicted :120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding :1179,1182,1785/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271-540/Domain:
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590-620 <MAN>
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                                                                                                                   I <DOM1>
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                                                                                                                                                                      alpha <ALP>
                                                                                                                                                                                                                              II <DOM2>
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EGF-like
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homology <LE13>
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                                                                                    (Gln) (in mature form) #status predicted
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Query Match

13 .08;

Score

36;

DВ ۲,

Length 1786;

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RESULT
S49160
hypothetical protein 14.5K - Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 16-Feb-1995 #sequence_revision 14-Jul-1995
                                                                                                                              В
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                                                                                                                                                                                                                                                                                             A; Map position:
C; Superfamily: F
                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A: Residues: 1-124 <VLC>
                                                                                                                                                                                                                                                                                                                                                                                                  R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of A;Reference number: Z14955; MUID:97404404
A;Accession: T03574
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Rhodobacter capsulatus C;Species: Rhodobacter capsulatus C;Date: 24-Mar-1999 #sequence_revision 24-Mar
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A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; FA; Title: Complete genome sequence of the methanogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: E64310
C;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton,
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C;Genetics:
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C;Genetics:
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A;Accession: E64310
                                     hypothetical
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Best Local S
Matches 4
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Matches 5; Conservative
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                                                                                                                                                                                                                       52.5%;
66.7%;
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83.3%;
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                                                                                                                                                                                                      0;
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Pred. No.
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 14-Jul-1995 #text_change
                                                                                                                                                                                                                       1.1e+02;
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   24-Nov-1999
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C; Accession: A39429
R; Kageyama, R.; Sasai, Y.; Nakanishi, S.
J. Biol. Chem. 266, 15525-15531, 1991
A; Title: Molecular characterization of transcription
A; Reference number: A39429; MUID:91332085
A; Accession: A39429
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-132 <NIE>
A;Cross-references: EMBL:226657; NID:g510211; PIDN:CAA81399.1; PID:g510213
C;Superfamily: Salmonella typhimurium hypothetical protein 14.5K
                       A;Cross-references: GB:M65148; NID:g206569; PIDN:AAA42013.1; PID:g206570 C;Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding C;Keywords: DNA binding; nucleus; transcription regulation C;Keywords: DNA binding; nucleus; transcription regulation F;231-271/Domain: fos/jun DNA-binding domain homology <FJD>
                                                                                                    A; Residues: 1-389 < KAG>
                                                                                                                                                                                                                                                                                       cAMP response element-binding protein ATF2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A; Introns: 57/3; 9
C; Superfamily: Scl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F22F7.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t C;Accession: T33188
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R; Nieweg, A.; Breme
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A; Residues: 1-195 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; 96/3; 160/2
Schizosaccharomyces pombe hypothetical protein SPBC31F10.03
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ce: strain Bristol N2; clone F22F7
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Pred. No. 2;
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A;Molecule type: mRNA
A;Residues: 1-486 <VII.>
A;Residues: 1-486 <VII.>
A;Cross-references: GB:U16158; NID:g887779; PIDN:AAA69518.1; PID:g710326
C;Comment: This protein is a sequence-specific DNA-binding protein that mediates tran C;Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain ho C;Keywords: leucine zipper; phosphoprotein; transcription regulation F;37-398/Region: leucine zipper motif F;329-359/Domain: fos/jun DNA-binding domain homology <FJD>
F;332-364/Region: basic
                                                                                                                                                                                                                                                                                                                                                     Gene 153, 225-229, 1995
A;Title: Analysis of ATF2 gene
A;Reference number: JC4028; MUI
A;Accession: JC4028
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1945
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70539
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                                                                                                       F:82/Binding site: phosphate (Ser) (covalent) (by protein kinase A) \#status F:102/Binding site: phosphate (Ser) (covalent) (by protein kinase C) \#status
                                                                                                                                                                                                                                                                                                                                                                                                                    R; Villarreal, X.C.; Richter, J.D. Gene 153, 225-229, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: cyclic AMP-response element-binding protein C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
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A; Residues: 1-451 <COL>
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A;Title: Deciphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
A;Accession: A70539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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Search completed: November 21, 2001, 15:46:55 Job time: 118 sec



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protein search, using sw model
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length: 2000000000
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Match Length DB
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Copyright (c) 1993 - 2000 Comp
2001,
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ATF2_MOUSE
ATF2_RAT
POLS_RUBV
YFH6_YEAST
                   HS7H_HUMAN
POLS_RUBVM
POLS_RUBVR
POLS_RUBVR
POLS_RUBVR
VI194_HUMAN
V1194_HUMAN
V1194_HUMAN
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49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	50.8	50.8	50.8
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FDNH_ECOLI	EGG1_SCHJA	EGG2_SCHJA	RL43_SCHPO	MT14_MYTED	MT13_MYTED	MT12_MYTED	MT11_MYTED	Y6KD_STRLI	RRPB_CVMA5	RRPB_CVMJH	VGLM_BUNSH
P24184 escherichia	P19470 schistosoma		094686 schizosacch	P80249 mytilus edu	P80248 mytilus edu	P80247 mytilus edu	P80246 mytilus edu	P22400 streptomyce	P16342 murine coro	P29982 murine coro	P04875 bunyavirus

ALIGNMENTS

RESULT _ C79A_MOUSE TD C79A_MOUSE T1911;

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requires a license agreement (See http://wan email to license@isb-sib.ch).	his SWISS-PROT entry is copyright. It is produced through a colletween the Swiss Institute of Bioinformatics and the EMBL ou he European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is it oddfied and this statement is not removed. Usage by and for	: 7.7	 -i- SUBUNIT: HETERODIMER OF ALPHA AND BETA CHAINS, DISULFIDE-LINKED. -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -i- TISSUE SPECIFICITY: B-CELLS. 	- I HUNDING PROFITED TO SURFACE IGM-RECEPTOR; MAY BE INVOLVED IN - SIGNAL TRANSDICTION.	"Molecular cloning of the Ig-alpha subunit of the human B-cell antigen receptor complex.";	MEDLINE-92347937; PubMed=1639443; MEDLINE-92347937; PubMed=1639443; Flaswinkel H., Reth M.;	(3)	J. Immunol. 145:337-343(1990).	"Structure of the murine mb-1 gene encoding a putative	Kashiwamura SI., Koyama T., Matsuo T., Steinmetz M., Kimoto M., Sakaguchi N.;		SEQUENCE FROM N.A.	ЕМВО J. 7:3457-3464(1988).	ted expression of mb	`_	STRAIN=C57BL/6 X DBA/2J;	SEQUENCE FROM N.A.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CD79A OR IGA OR MB-1. Mus musculus (Mouse).		PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED	GEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN	15-JUL-1999 (Rel. 38, Last annotation update)	(Rel. 12,	C79A_MOUSE STANDARD; PRT; 220 AA. P11911;

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FRESULT FRESUL
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           "Ectopic neural expression of a floor plate arker in frog embryos injected with the midline transcription factor Pintallavis.";

Proc. Natl. Acad. Sci. U.S.A. 90:8268-8272(1993).

- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY CONTRIBUTE. TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL CONTRIBUTE. TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL CONTRIBUTE.
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MEDLINE=93376785; PubMed=8367492;
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CONFLICT
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Amphibia; Batrachia; Anura; Me
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Xenopus laevis (African clawed frog).
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SIGNAL 1
CHAIN 23
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                                     PIR; A47723; A47723.
InterPro; IPR000884; -.
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TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS
SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
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A43540;
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M31773; AAA39494.1;
S01648; S01648.
                                                                            L09123; AAA19105.1;
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N-LINKED (G)
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
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1-LINKED (GLCNAC. ..) (POTENTIAL).
GACTG -> HRGLYW (IN REF. 3).
A654123C58177B29 CRC64;
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LAR (POTENTIAL).
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CHAIN DOMAIN

POTENTIAL. F-SPONDIN. TSP TYPE-1

Cell adhesion

Pfam; PF02014; Reeler; 1.
Pfam; PF00090; tsp_1; 6.
PROSITE; PS50092; TSP1; 5.
Glycoprotein; Signal; Repeat;
SIGNAL 1 28

InterPro; IPR000884; -. InterPro; IPR002861; -.

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FSPO_RAT
ID PSPO
AC P354
DT 01-J
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CC EUKE
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01-JUN-1994 (Rel. 29)
01-OCT-2000 (Rel. 40)
F-SPONDIN PRECURSOR.
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eithe European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klar A., Baldassare M., Jessell T.M.; "F-spondin: a gene expressed at high levels in the floor plate encodes a secreted protein that promotes neural cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                EMBL; M88469; AAA41174.1; PIR; A38152; A38152.
                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurite extension.";
Cell 69:95-110(1992)
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Mammalia; Eutheria;
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Rnkarvota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS
SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE S
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(Rel. 29, Last sequence up
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192; TSP1;
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83.3%;
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Sciurognathi; Muridae;
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Pfam; PFO()
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                         aggregation.";
J. Cell Sci. 109:1053-1061(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ependymocyte;
MEDLINE=96338614; PubMed=8743952;
Gobron S., Monnerie H., Meiniel R.,
Lamalle D., Dastugue B., Meiniel A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
SCO-SPONDIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSPO_BOVIN P98167;
                                                                                                                                     EMBL; X93922; CAA63815.1; HSSP; P01130; 1AJJ.
                                                                                                                                                                         or send
                                                                                                                                                                                                                                                                                                                                                                                                                "SCO-spondin: a new member of the thrombospondin family so the subcommissural organ is a candidate in the modulation
                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
DEVELOPMENTAL STAGE: EMBRYO.
SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taurus (Bovine).
          srPro; IPR000421; ...
srPro; IPR001007; ...
srPro; IPR001107; ...
srPro; IPR002172; ...
srPro; IPR002219; ...
srPro; IPR002519; ...
srPr00754; F5_F8_type_C; 1
spF01826; TIL; 1.
spF01826; TIL; 1.
spF01826; tSp_1; 4.
spF00093; vwc; 1.
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309525F9EAFEA89A CRC64;
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ed. No. 22;
Mismatches
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P07942;
01-AUG-1988 (Rel. 08, 0
01-AUG-1988 (Rel. 08, 1
01-OCT-2000 (Rel. 40, 1
LAMININ BETA-1 CHAIN PI
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-87280097; PubMed-3611077;

MEDLINE-87280097; PubMed-3611077;

Pikkarainen T., Eddy R., Fukushima Y., Byers M., Shows T.,

Pikhlajaniemi T., Saraste M., Tryggvason K.;

Pihlajaniemi T., Saraste M., Tryggvason K.;

Pihlajaniemi T., Saraste M., Tryggvason K.;
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DOMAIN
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MEDLINE=90388768; PubMed=1975589;

Vuolteenaho R., Chow L.T., Tryggvason K.;

"Structure of the human laminin Bl chain gene.";

J. Biol. Chem. 265:15611-15616(1990).
                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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PS01209;
PS50068;
PS50092;
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Last annotation updat
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(LAMININ B1 CHAIN).
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the Euro
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-! SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-2 (MEDGIN), AND LAMININ-6 (K-LAMININ-1 (EHS LAMININ), LAMININ-2 (MEGELULAR LOCATION: EXTRACELLULAR.

-! TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

-! DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

-! SIMILARITY: CONTAINS 1 LAMININ N-TERRINAL DOMAIN (DOMAIN VI).

-! SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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Jaye M., Modi W.S.,
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                                                                                                    SEQUENCE OF 1292-1786 FROM N.A. MEDLINE-85051302; PubMed-6209134; BARTLWNE-PS. Green N.M., Kurkinen M., "Sequencing of laminin B chain cDNAs coiled-coil alpha-helix."; EMBO J. 3:2355-2362(1984).
                                                                                                                                                                                                                                                    MEDLINE=87147212; PubMed=3493487;
Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
"Sequence of the cDNA encoding the laminin B1 chain rev
multidomain protein containing cysteine-rich repeats.";
Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).
SEQUENCE OF 165-172; 539-547 AND 712-719
STRAIN-BALB/C; TISSUE-Endothelial cells;
MEDLINE-97363207; PubMed-9219532;
Frieser M., Noeckel H., Pausch F., Roeden
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PRINTS; PR00011; EGFLAMININ.
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EUR. J. BIOCHEM. 246:727-735(1997).

FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS LATO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHOND WITH GLOBULES AT EACH END. THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-2 (MEROSIN), AND LAMININ-6 (K-LAMININ).

SUBCELLULAR LOCATION: EXTRACELLULAR.

-I- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

-I- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

-I- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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EMBL; X05212; CAA28839.1;
PIR; A26413; MMMSB1.
HSSP; P03069; 1ZIM.
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European
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PS01186;
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EGF_2;
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LAMININ N-TERMINAL (DOMAIN VI).

4.5 X LAMININ EGF-LIKE REPEATS

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hesion; Repeat; Signal.
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SEQUENCE FROM N.A. MEDLINE-87147212; NCBI_TaxID=10090; [1] Eukaryota; Metazoa; Mammalia; Eutheria;

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FF2_CHICK STANDARD; PRT; 487 AA.

O33602;

O30-MAY-2000 (Rel. 39, Created)

O-MAY-2000 (Rel. 39, Last sequence update)

O-MAY-2000 (Rel. 39, Last annotation update)

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-2

TRANSCRIPTION FACTOR 2).
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chord
Archosauria; Aves; Neogna
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

Jannaschii.";

Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There muse by non-profit institutions as long as its c modified and this statement is not removed. Usage entities requires a license agreement (See http://w
SEQUENCE FROM N.A. Huguier S., Baguet J., "Transcription factor.
                                                                           NCBI_TaxID=9031;
[1]
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Pfam; PF01497; Peripla_BP_2;
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TIGR; MJ0085;
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01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-2 (ACTIVATING TRANSCRIPTION FACTOR 2) (CAMP RESPONSE ELEMENT BINDING PROTE
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MEDLINE=90205810; PubMed=2320002; Kara C.J., Liou H.-C. Twanking
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                                                                                                                                    Maekawa T., Sakura H., Kanei-Ishii C., Su
Fujisawa J.I., Yoshida M., Ishii S.,
"Leucine zipper structure of the protein
cyclic AMP response element in brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PSO0036; BZIP_BASIC; 1.

PROSITE: PSO0028; ZINC_FINGER_C2H2_1; 1.

PROSITE: PS50157; ZINC_FINGER_C2H2_2; 1.

Transcription regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P15336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y17724; CAA76838.1;
HSSP; P08047; 1SP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vivo.
                                                                                                                    EMBO J.
                                                                                                                                                                                                                                              MEDLINE=90005408; PubMed=2529117;
                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATF2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000822;
InterPro; IPR001871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: A TRANSCRIPTIONAL ACTIVATOR, PROBABLY CONSTITUTIVE,
WHICH BINDS TO THE CAMP RESPONSIVE REGION (CRE) (CONSENSUS:
5'GTGACGT(A/C)(A/C)); A SEQUENCE PRESENT IN MANY VIRAL AND
CELLULAR PROMOTERS (BY SIMILARITY).
SUBUNIT: BINDS DNA AS A DIMER.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CXGPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR CREB2 OR CREBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HB16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00170; bZIP; 1.
PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         independent proliferation in vitro and
                                                                                                                 8:2023-2028(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333
362
487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356
390
                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.5%;
66.7%;
          Ivashkiv L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
BASIC MOTIF.
LEUCINE-ZIPPER.
; A1F42734D9C6A146 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
             Glimcher L.H.;
                                                                                                                                                                                                                      Sudo T., Yoshimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                  CRE-BP1 binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN CRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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В
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                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                   MOUSE
ATF2_MOUSE
STANDARD; PRT; 487 AA.
P16951; 064089; 064090; 064091;
01-AUG-1990 (Rel. 15, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-2 (ACTIVATING TRANSCRIPTION FACTOR 2) (CAMP RESPONSE ELEMENT BINDING PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15875; CAA33886.1; -. EMBL; M31630; AAA35951.1; -. PIR; S05380; S05380. HSSP; P08047; ISP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A CDNA for a human cyclic AMP response element-binding is distinct from CREB and expressed preferentially in br Mol. Cell. Biol. 10:1347-1357(1990).

-i- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEME
 SEQUENCE OF 9-487 FROM N.A.,
                         NCBI_TaxID=10090;
                                         Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                          15 CXGPGC
                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
(CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN M.
VIRAL AND CELLULAR PROMOTERS.
SUBUNIT: BINDS DNA AS A DIMER.
SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: MXBP AND CRE-BP1 MAY BE MEMBERS OF A F/A
OF MXBP/CRE-BP PROTEINS GENERATED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ABUNDANT EXPRESSION SEEN IN THE BRAIN.
PTM: PHOSPHORYLATION OF THR-69 AND THR-71 BY MAPK14 CAUSES
THE PROPERTY OF THR-69 AND THR-72 BY MAPK14 CAUSES
THE PROPERTY OF THR-69 AND THR-72 BY MAPK14 CAUSES
                                                                    musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.
                                                                                              (MXBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATED BY JNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCREASED TRANSCRIPTIONAL ACTIVITY. ALSO PHOSPHORYLATED
                                                                                                                                                                                                                                                                CTAPGC
                                                                                                                                                                                                                                                                                                                     Similarity
4; Conserv
                                         ; Metazoa;
Eutheria;
                                                                                               PROTEIN).
                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                    (Mouse)
                                         Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                   52.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                      0,:
                                                                                                                                                                                                                                                                                                                                   Score
Pred.
  AND ALTERNATIVE SPLICING
                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                  e 31; DB 1; Lc...
1. No. 1.1e+02; Lc...
2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PRESENT IN MANY
                                          Muridae;
                                                                                                                                                                                                                                                                                                                                              Length 487;
                                                                                                                                                                                                                                                                                                                      Indels
                                                         Euteleostomi;
                                          Murinae;
                                                                                                               PROTEIN CRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein which
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A FAMILY
                                            Mus
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      0;
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MEDLINE=92123199; PubMed=1531087;

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R MGD; MGI:10934y; ...

R MGD; MGI:10934y; ...

R MGD; MGI:10934y; ...

InterPro; IPR00082; -.

DR InterPro; IPR001871; -.

DR Pfam; PF00170; bZIP; 1.

DR Pfam; PF00170; bZIP; 1.

DR PROSITE; PS00036; BZIP_BASIC; 1.

DR PROSITE; PS00038; ZINC_FINGER_C2H2_1; 1.

DR PROSITE; PS00038; ZINC_FINGER_C2H2_2; 1.

Transcription regulation; DNA-binding; Activator; Phosphorylation; C2H2-TYPE.

C2H2-TYPE.

Table 1.

Table 2.

Table 3.

Table 4.

Table 4.
QΥ
                                                                                                                                                                   Query Match
Best Local
                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S76657; AAB21128.1; A
EMBL; S76659; AAB21127.1; A
EMBL; S76655; AAB21127.1; -
EMBL; M31629; AAA39780.1; -
PIR; A34785; A34785
HSSP; P03069; 2DGC.
                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ivashkiv L.B., Liou H.-C., Kara C.J.,
Glimcher L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georgopoulos K., Morgan B.A., Moore D.D.;
"Functionally distinct isoforms of the CRE-BP DNA-binding protein mediate activity of a T-cell-specific enhancer.";
Mol. Cell. Biol. 12:747-757(1992).
                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        element.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 77-487 FROM N.A
                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90205841; PubMed=2138707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "mXBP,
    15 CXGPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF AN MXBP-C-JUN COMPLEX.
SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM A HOMODIMER ABSENCE OF DNA. CAN FORM AN HETERODIMER WITH C-JUN.
SUBCELLOLAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AN PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: A TRANSCRIPTIONAL ACTIVATOR, PROBABLY CONSTITUTIVE, WHICH BINDS TO THE CAMP RESPONSIVE REGION (CRE) (CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'); A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. THE INTERACTION OF MXBP/CRE-BB2 WITH C-JUN REDIRECTS C-JUN TO BIND TO CRES PREFERENTIALLY OVER THE 12-0-TETRADECANOXLDHORBOL-13-ACETATE RESPONSE ELEMENTS (TRES) AS PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not to the 12-0-tetradecanoylphorbol-13-acetate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /CRE-BP2 and c-Jun form a complex which binds to
                                                                     Similarity
    20
                                                  Conservative
                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10:1609-1621(1990)
                                                                                                                                                              229
487
52297
                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                          53
                                                                     52.5%;
66.7%;
                                                                                                                                                                   Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALT_INIT.
                                                0;
                                                                   Score 31; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                             SIMILARITY).

PHOSPHORYLATION (BY MAPK14) (BY SIMILARITY).

MSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFGPAR
                                                                                                                                                              NDSVIVA -> MHCPWVWP (IN ISOFORM MISSING (IN GEOROM 2).
AQPSGS -> HSPQEVD (IN REF. 1).
F9CDEC3BC3119ACB CRC64;
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamph W.W.,
                                                                                           Length 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N HOMODIMER
I C-JUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Verma I.M.,
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InterPro; IPR000822; ...
InterPro; IPR001871; ...
Pfam; PF00170; bZIP; 1.
Pfam; PF00096; zf-C2H2; 1.
                                                                                                            PROSITE; PS00036; BZIP_BASIG; 1.

PROSITE; PS00036; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.

Transcription regulation; DNA-binding; Activator; Phosphorylation; Nuclear protein; Alternative Splicing; Zinc-finger; Metal-binding.
VARSPLIC
SEQUENCE
                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kageyama R., Sasai Y., Nakanishi S., "Molecular characterization of transcription factors that CAMP responsive region of the substance P precursor gene. cloning of a novel C/EBP-related factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATF2_RAT STANDARD; PRT; 487 AA. Q00969; Q62870; Q1-APR-1993 (Rel. 25, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-2 (ACTIVATING TRANSCRIPTION FACTOR ATF-2) (CAMP RESPONSE ELEMENT BINDING PROTE
                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                         MOD_RES
                                                                                                                                                                                                                                                                 HSSP; P08047; 1SP2
                                                                                                                                                                                                                                                                             PIR; A39429; A39429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91332085; PubMed=1714459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
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CELLULAR PROMOTERS.

SUBUNIT: BINDS DNA AS A DIMER.

SUBCELLULAR LOCATION: NUCLEAR.

SUBCELLULAR LOCATION: SUBCEAR, 1 (SHOWN HERE) AND 2;

ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2;

PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.

SIMILARITY: BELONGS TO THE BZIP FAMILY.
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TISSUE=Brain;
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                                                                                 BASIC MOTIF.
LEUCINE-ZIPPER
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Sciurognathi; Muridae;
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P43590;
01-NOV-1995
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SEQUENCE
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CHAIN
SIGNAL
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-i- FUNCTION: GLYCOPROTEIN El CONTAINS THE VIRAL HEMAGGLUTIN
                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1.1e+02;
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Matches 4
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P34931; Q9UQM1;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                            SEQUENCE FROM N.A.
MEDLINE=91055806; PubMed=1700760;
Milner C.M., Campbell R.D.;
"Structure and expression of the
                                                                                                                                       Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Finance; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murakami Y., Naitou M., Hagiwara H.,
Sasanuma S.-I., Sasanuma M., Tschiya
Sasanuma S.-I., Eki T.,
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
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Hypothetical protein; Hydrolase; Transmembrane.
TRANSMEM 8 24 POTENTIAL.
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SGD; S0001902; YFR006W.
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 Rowen L.,
Loretz C.,
                           SEQUENCE FROM
                                                                                                                                   NCBI_TaxID=9606;
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InterPro; IPR001131; -.
Pfam; PF00557; Peptidase_M24; 1.
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ROM N.A.
Qin S., Madan A.,
Ratcliffe A., Ab
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                                                     expression of the 32:242-251(1990).
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PEPTIDASE IN MPR1-GCN20
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 Dickhoff R., Dors M.,
basi N., Shaffer T., H
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Pred. No. 1.1e+02
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a Y., Soeda
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               Madan A.,
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MIM; 140559; -.
InterPro; IPR001023; -.
Pfam; PP00012; HSP70; 1.
PF10012; HSP70; 1.
PROSITE; PR00301; HEATSHOCK70.
R PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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01-AUG-1988 (Rel. 0
01-AUG-1988 (Rel. 0
11-JUL-1998 (Rel. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                        MEDLINE-8717/4825; PubMed=3562245; Clarke D.M., Loo T.W., Hui I., Chong P., Gillam S.; "Nucleotide sequence and in vitro expression of rubella visuagenomic messenger RNA encoding the structural proteins
                                                                                                                        SEQUENCE FROM N.A. MEDLINE-87174825;
                                                                                                                                                                                                                   GLYCOPROTEINS E1 AND E2]
Rubella virus (strain M3
                                                                                                                                                                                                  Rubella virus (strain M33).
Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                               RUBVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milner C.M., Campbell R.D.;
"Polymorphic analysis of the three MHC-linked HSP70 genes.";
Immunogenetics 36:357-362(1992).
-i- INDUCTION: NOT INDUCED BY HEAT SHOCK.
-i- MISCELLANEOUS: ENCODED IN THE MHC-III COMPLEX.
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                Nucleic Acids
                                                                                                                                                                                                                                                   STRUCTURAL POLYPROTEIN
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                                                                                                                                                                       NCBI_TaxID=11043;
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PIR; B45871; B45871.
HSSP; P19120; 1NGJ.
MIM; 140559; -.
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SUMMARIES

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A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833 A;Accession: B82503

A;Cross-references: GB:AE004351; GB:AE003853; NID:g9657462; PIDN:AAF95998.1; GSPDB:GN A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor

C; Genetics:

A; Gene: VCA0084

A; Molecule type: DNA A; Residues: 1-148 <HEI>

A;Status: preliminary

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I., R.R.; Mekkalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

Gwinn, M.L.; Dodson, R. H.; Dragoi, I.; Sellers

C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82503

soxR protein VCA0084 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
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ALIGNMENTS

A;Residues: 1-156 <STO>
A;Cross-references: GB:AE004653; GB:AE004091; NID:g9948298; PIDN:AAG05661.1; A;Experimental source: strain PAO1
C;Genetics: 믕 Qy A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: B83361 A; Status: preliminary A; Molecule type: DNA Query Match
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Matches 10; Conserv 7 GCIGPGCACLQAC 19 |||| || ||| 116 GCIGCGCLSLQAC 128 Conservative 46.78; 76.98; 0; Score 57; Pred. No. Mismatches DB 1.1; 2: ω •• Length 156; Indels 0 Gaps GSPDB:GN 0,

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A;Reference number: S39416; MUID
A;Accession: S39418
A;Molecule type: protein
A;Residues: 1-72 cMAC>
C;Superfamily: metallothionein
C;Keywords: metal binding
                                                                            metallothionein 10-IV - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
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R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Bur. J. Biochem. 218, 183-194, 1993
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A;Residues: 1-72 <MAC>
C;Superfamily: metallothionein
C;Keywords: metal binding
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
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R;Mackay, E.A.; Overnell, J.; Dunbar, B.;
                 Eur. J. Biochem. 218, 183-194
A; Title: Complete amino acid
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                                                 Hunziker, P.E.; Kaegi, J.H.R.;
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               four monomeric
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R:Sakaguchi, N.; Kashiwamura, S.; Kimoto, M.; Thalmann, P.; Melchers, F.
EMBO J. 7, 3457-3464, 1988
A;Title: B lymphocyte lineage-restricted expression of mb-1, a gene with CD3-like str
A;Reference number: S01648; MUID:89091088
A;Accession: S01648
A;Accession: S01648
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-220 <SAK>
A;Cross references: EMBL:X13450; NID:g53015; PIDN:CAA31801.1; PID:g53016
R;Hombach, J.; Lottspeich, F.; Reth, M.
Eur. J. Immunol. 20, 2795-2799, 1990
                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KAS>
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S39417
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A;Residues: 1-72 <MAC>
C;Superfamily: metallothionein
C;Keywords: metal binding
A; Reference number: A60228; A; Accession: A60228
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 05-Nov-1999 (;Accession: A43540; S01648; A60228; A39398; I57521 R;Kashiwamura, S. I.; Koyama, T.; Matsuo, T.; Steinmetz, M.; Kimoto, M.; Sakaguchi, N. J. Immunol. 145, 337-343, 1990
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A; Residues: 1-72 < MAC>
C; Superfamily: metallothionein
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C; Species: Mytilus edulis (blue mussel)
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                                              A; Title: Identification
                                                                                                                                                                                                                                                                       A;Cross-references: GB:M31773; NID:g199032; PIDN:AAA39494.1; PID:g387413 R;Sakaguchi, N.; Kashiwamura, S.; Kimoto, M.; Thalmann, P.; Melchers, F.
                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A43540
                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Structure of the murine mb-1 gene encoding a putative sigM-associated molecu A; Reference number: A43540; MUID: 90293481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: surface IgM complex alpha chain
C;Species: Mus musculus (house mouse)
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A;Accession: S39417
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                         of the genes encoding 228; MUID:91099432
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A; Molecule type: protein A; Residues: 29-38 < HOM>

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aptotoxin III - trap-door spider (Aptostichus sp.)
N.Alternate names: insecticidal peptide Aps III
C; Species: Aptostichus sp.
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
C; Accession: E44007
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaels, Recession: H69421
A;Recession: H69421
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C;Accession: H69421
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Fleischmann, R.D.; Querbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
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A:Residues: 'X', 30-38 <CAM>
R:Travis, A.; Hagman, J.; Grosschedl, R.
Mol. Cell. Biol. 11, 5756-5766, 1991
A:Title: Heterogeneously initiated transcription from the A:Reference number: I57521; MUID:92017857
A:Accession: I57521
                        R; Skinner, W.S.; Dennis, P. Toxicon 30, 1043-1050, 1992
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A; Residues: 1-659 <KLE>
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A;Title: IgM antigen receptor complex contains phosphoprotein products of A;Reference number: A39398; MUID:91219496
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A; Residues: 1-15, 'QA' <RES>
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Identification of insecticidal peptides from venom
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                                             P.A.; Li, J.P.; Quistad,
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26;
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  of the trap-door spider,
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein NMB1825 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: F81037
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A; Accession: E44007
A; Molecule type: protein
A; Residues: 1-37 <SKI>
                                     A;Cross-references: GB:AL162753;
A;Experimental source: serogroup
                                                                               A; Molecule type: DNA
A; Residues: 1-71 <PAR>
                                                                                                                                           A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556
A;Accession: D81983
                                                                                                                                                                                                            C;Accession: D81983
R;ParKhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quall, M.A.; Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                hypothetical protein NMA0634 [imported] - Neisseria meningitidis (strain 22491 serogr C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: NMB
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A;Experimental source: serogroup
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A; Residues: 1-67 <TET>
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A;Accession: F81037
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A;Note: the source is designated as Aptostichus schlingeri
A;Note: sequence extracted from NCBI backbone (NCBIP:11952
C;Keywords: disulfide bond; toxin; venom
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9; Conser
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56.2%;
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                                     GB:AL157959; NID:g7379120; PIDN:CAB83924.1; A, strain Z2491
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Pred. No. 8.6;
1; Mismatches
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Pred. No. 4.1;
1; Mismatches
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Rajandre
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Query Match

39.38;

Score

48;

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Length 71;

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probable RNA-directed RNA polymerase (EC 2.7.7.48) - southern bean mosaic vi C;Species: southern bean mosaic virus, SBMV C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-Jun-1999 C;Accession: B33739 R;Wu, S.; Rinehart, C.A.; Kaesberg, P. Virology 161, 73-80, 1987 P. Virology 161, 73-80, 1987 P. P. Title: Sequence and organization of southern bean mosaic virus genomic RNA A;Reference number: A33739; MUID:88044510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56K serine proteinase (EC 3.4.21.-) - ictalurid herpesvirus 1 (strain C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun C;Accession: C36791
R;Davison, A.J.
submitted to GenBank, January 1992
A;Description: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A36804
                                                                                                                                                                          A; Molecule type: genomic RNA
A; Residues: 1-956 <WUS>
A; Residues: 1-956 <WUS>
A; Cross-references: GB: M23021; NID:g511859; PIDN:AAA46565.1; PID:g511861
C; Superfamily: potato leaf roll virus RNA-directed RNA polymerase
C; Keywords: nucleotidyltransferase; RNA biosynthesis
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Best Local Similarity
"~+~hes 8; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 186, 9-14, 1992
A;Title: Channel catfish virus: a new type
A;Reference number: A39447; MUID:92087490
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A; Residues: 1-518 <DAV>
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8; Conserv
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1; Mismatches
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Pred. No. 64;
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Pred. No. 40;
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RESULT

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Search completed: Job time: 117 sec

November 21,

2001,

15:46:54

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hypothetical protein 12 - equine herpesvirus 2
C. Species: equine herpesvirus 2
C. Species: equine herpesvirus 2
C. Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C. Accession: S55608
R. Telford, E. A. R.; Watson, M. S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A; Title: The DNA sequence of equine herpesvirus 2.
A; Reference number: S55594; MUID:95302501
                                                                                                                                                                             A;Cross-references: GB:AE005174; NID:g12516435; PIDN:AAG57262.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-385 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; transla A;Molecule type: DNA A;Molecule type: DNA A;Moslecule type: DNA A;Moslecule type: DNA A;Residues; 1-161 <TELD A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13801.1; PI A;Note: the nucleotide sequence was submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: B85850
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C; Accession: B85850
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C; Species: Escherichia coli
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57.1%;
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MUID:21074935; PMID:11206551
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La Library, February
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K.; Apoda
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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EMBL; X95517; CAA64771.1; -. EMBL; AE004653; AAG05661.1; -.

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ALIGNMENTS

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Y95517: CAA64771 1: -	or send an email to license@isb-sib.ch).	" : 	modified and this statement is not removed. Heage by and for commercial	here are no restrictions on	informatics and the EMBL outstatic	This SWISS-PROT entry is copyright. It is produced through a collaboration			- i - SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL	ī		TRANSCRIPTIONAL ACTIVITY OF SOXR IN RESPONSE TO SPECIFIC TYPES OF	CHISTER MAY THIS BE EMPLOYED IN VIVO TO MODILLATE THE	THAT RECOGNIZES SUPEROXIDE. THE VARIABLE REDOX STATE OF THE FE-S.	TIBELS CONINCE THE SUFFERNATIONS RESCOUNT BOOK OCCUPANT OF STREET		Nature 406:959-964(2000).	opportunistic pathogen.";	"Complete genome sequence of Pseudomonas aeruginosa PAO1, an	Reizer J. Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,	Smith K.A. Spencer D.H. Wong G.KS. Wu Z., Paulsen I.T.,	Rrody I. I. Coulter S. W. Folger K. R. Kas A. Larbig K. Lim R. M.	attrey mil., bilinian milation F. Westhrock-Wadman S. Vian V., Garber B. Golfry I. Tolentino F. Westhrock-Wadman S. Vian V.	Stover C.K., Pham XQ.T., EFWID A.L., MIZOGUCHI S.D., WAITCHEF P., UICHON M T DEFINION F C T UNFRAGE W O VOUGHIER D T TEATON M	MEDLINE=20437337; PubMed=10984043;	STRAIN=PAO1;	SEQUENCE FROM N.A.		J. Bacteriol. 179:1490-1496(1997).	exemplifying actualinose, dene crountly and drower brace debendence by the crountly and drower brace debendence	and growth	3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		STRAIN-ATCC 15692 / PAO1;	SEOUENCE FROM N.A.	NCBI_TaxID=287;		Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	SOXR OR PA22/3.	REDOX-SENSITIVE TRANSCRIPTIONAL ACTIVATOR SOXR.	(Rel	01-NOV-1997 (Rel. 35, Last sequence update)) j	ID SOXR_PSEAE STANDARD; PRT; 156 AA.		

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RESULT

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DT O:

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      RESULT
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01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
01-NOV-1997 (Rel. 3
                                                                                                                                                                      MT12_MYTED P80247; 01-FEB-1994
                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
METALLOTHIONEIN 10-II (MT-10-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJINE-94062828; PubMed=8243463;
MEDIJINE-94062828; PubMed=8243463;
Mackay E.A., Overnell J., Dunbar B., Davidson I.
Kaegi J.H.R., Fothergill J.E.;
"Complete amino acid sequences of five dimeric a forms of metallothionein from the edible mussel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001008; -.
Interpro; IPR003019; -.
Pfam; PP00131; metalthio; 1.
PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Chelation;
SEQUENCE 72 AA; 7105 MW; 3EA99D959AEEB3B2 CRCf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 218:183-194(1993).
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED
SEQUESTRATION OF TOXIC METAL IONS.
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Pfam; PF00376; merr; 1.
PRINTS; PR00040; HTHMERR.
PROSITE; PS00552; HTH MERR FAMILY; 1.
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                         MYTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METALLOTHIONEIN 10-I (MT-10-I).
Mytilus edulis (Blue mussel).
Eukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Transcription regulation; Activator; Iron-sulfur.

DNA_BIND 12 31 H-T-H MOTIF (POTENTIAL).

DOMAIN 117 128 MIGHT BE PART OF A SENSOR REGION.

SEQUENCE 156 AA; 16998 MW; 7B542A23804D72C2 CRC64;
                                            Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- INDUCTION: BY CADMIUM.
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; P15358; 1SKZ.
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                                        edulis (Blue mussel)
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of Mytilus
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edulis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
InterPro; IPR001008; -.
InterPro; IPR003019; -.
Pfam; PF00131; metalthio; 1.
PRINTS; PR00875; mYMMOLLUSC.
Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
SEQUENCE 72 AA; 6949 MW; 648AF4576E80726E CRC64;
                                                                                                                                   "Complete amino acid sequences of five forms of metallothionein from the edibl Eur. J. Blochem. 218:183-194(193).
-i- FUNCTION: THE METALLOTHIONEINS ARE SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
METALLOTHIONEIN 10-III (MT-10-III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0875; MTMOLLUSC.

PRINTS; PRO0875; METAL-thiolate cluster; Chelation; Ca
Metal-binding; Metal-thiolate cluster; Chelation; Ca
SEQUENCE 72 AA; 7036 MW; 7FA99D959AEEB269 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 218:183-194(1993).
-!- FUNCTION: THE METALLOTHIONEINS ARE SEQUESTRATION OF TOXIC METAL IONS.
                                                                         PIR; S39418; S39418.
HSSP; P04355; 4MT2.
                                                                                                                                                                                                Mackay E.A., Overnell J., Dunba
Kaegi J.H.R., Fothergill J.E.;
                                                                                                                                                                                                                                                            Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                    Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001008; -.
InterPro; IPR003019; -.
Pfam; PF00131; metalthio;
                                                                                                  -!- INDUCTION: BY CADMIUM.
                                                                                                                         -!- SUBUNIT: MONOMER
                                                                                                                                                                                                             MEDLINE=94062828; PubMed=8243463; Mackay E.A., Overnell J., Dunbar B.,
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               P80248;
                                                                                                                                                                                                                                                                                                                                                                           MT13_MYTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   forms of metallothionein from the edible mussel Myt Eur. J. Biochem. 218:183-194(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mackay E.A., Overnell J., Dunbar B., Da Kaegi J.H.R., Fothergill J.E.; "Complete amino acid sequences of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S39417; S39417.
HSSP; P15358; 1SKZ.
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Query Match Best Local S Matches 8

Similarity 8; Conser

Conservative

41.0%; 61.5%;

9: Score 50; DB Pred. No. 0.87 0; Mismatches

.87;

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Gaps

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Length 72;

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GCIGPGCACLQAC

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RESULT 6
C79A_MM
AC P11911
DT 01-OCT
DT 01-OCT
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DE B-CELL
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DE ASSOCI
DE PROTEI
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Best Local 9
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01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
01-NOV-1997 (Rel. 2
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                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN
PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM-
ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED
                                                                                                                                                                                                                                                               C79A_MOUSE
P11911;
STRAIN-C57BL/6 X DBA/2J;
MEDLINE-89091088; PubMed=2463161;
Sakaguchi N., Kashiwamura S., Kimoto M., Tha
"B lymphocyte lineage-restricted expression
like structural properties.";
EMBO J. 7:3457-3464(1988).
                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                           CD79A OR IGA OR MB-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate
SEQUENCE 72 AA; 6979 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- INDUCTION: BY CADMIUM.
-!- SIMILARITY: BELONGS TO PIR; S39419; S39419.
HSSP; P04355; 4MT2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mackay E.A., Overnell J., Dunbar B., Kaegi J.H.R., Fothergill J.E.; "Complete amino acid sequences of fiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METALLOTHIONEIN 10-IV (MT-10-IV).
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                                                                              SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94062828; PubMed=8243463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ms of metallothionein from the edible mussel . J. Biochem. 218:183-194(1993).
FUNCTION: THE METALLOTHIONEINS ARE INVOLVED SEQUESTRATION OF TOXIC METAL IONS. SUBBRIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                      GCIGPGCACLQAC
                                                                                                                                                                                                                                                                                                                                              GCSGEGCRCGDAC
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                         (CD79A)
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                              STANDARD;
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. 28, Last sequence 35, Last annum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY
                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB
Pred. No. 0.87
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             range cluster; Chelation; Cadmium 7FA028637D837269 CRC64;
                                                                                                                  Craniata; Veri
Sciurognathi;
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                                         Kimoto M., Thalmann
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0.87;
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                            gene with
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RESULT
TXP3_AF
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Best Local
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TXP3_APTSC STANDARD; PRT; 37 AA. P49268; P49268; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) O1-FEB-1996 (Rel. 33, Last annotation update) APTOTOXIN III (PARALYTIC PEPTIDE III) (PP III). Aptostichus schlingeri (Trap-door spider). Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
                                                                                              _APTSC
                                                                                                                                                                                                                                                  CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation.
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S01648; S01648.
PIR; A43540; A43540.
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"Molecular cloning of the Ig-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-92347937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sIgM-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90293481; PubMed=2358676; Kashiwamura S.-I., Koyama T., Mat
                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: ASSOCIATED TO SURFACE IGM-RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the murine mb-1 gene encoding a putative sigM-associated molecule.";
J. Immunol. 145:337-343(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakaguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                   mmunoglobulin domain;
                                                                                                                                            15
                                                                                                                                                                  2 VYESWGCIGPGCACLQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: B-TELLS.
PTM: PHOSPHORYLARED ON TYLOSINE AS A RESULT OF B-CE
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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                                                                                                                                            LFLSYACLGPGCQALR
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                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                               23
138
160
43
50
113
58
68
                                                                                                                                                                                          Conservative
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159
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220
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43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                   WW.
                                                                                                                                                                                                     Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOP C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN TGACTG -> HRGLYW (IN REF. 3).
                                                                                                                                                                                                                                                                                              INTERCHAIN (TO BETA-CHAIN)
                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED PROTEIN ALPHA-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                  B-CELL ANTIGEN RECEPTOR COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsuo T.,
                                                                                                                                                                                                                                                     A654123C58177B29
                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                     DВ
2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ong as its content is in
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                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                 Length 220
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IYPE DOMAIN.
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                              VG47_HSVI1 STANDARD; PRT; 518 AA Q00139; Q00139; (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) 56 KDA SERINE PROTEASE (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; ACT_SITE
                                           PROSITE;
                                                               PIR; C36791; PRBEI1.
InterPro; IPR000209; -.
InterPro; IPR002884; -.
Pfam; PF01483; P; 1.
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                         Ictalurid herpesvirus 1 (Channel catfish virus)
Viruses; dsDNA viruses, no RNA stage; Herpesviri
unclassified Herpesviridae.
                                                                                                        EMBL; M75136; AAA88150.1;
                                                                                                                                                                                                                          Virology 186:9-14(1992).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=AUBURN 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93069259; PubMed=1440641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mygalomorphae; Cyrtaucheniidae; Aptostichus.
NCBI_TaxID=12944;
                                  PROSITE;
                                                                                                                                                                                                                                                                    MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venom;
                                                                                                                                                                                                                                                  "Channel catfish virus:
                                                                                                                                                                                                                                                            Davison A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YESWGCIGPGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNVWNCIGGGCS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toxin
                                PS00136;
PS00137;
PS00138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
            Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 AA;
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 ΑA;
                                ; SUBTILASE_ASP;
; SUBTILASE_HIS;
; SUBTILASE_SER;
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  55984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.2%;
58.3%;
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                                                                                                                                                                                                                                               new type of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1
Pred. No. 0.7;
1; Mismatches
 CHARGE RELAY SYSTEM (BY SIMILARITY)..;
DAAAF919A975460D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBD01091694E1908
                               FALSE_NEG.
FALSE_NEG.
                                                                                                                                                                                                                                               herpesvirus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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Best Local S
Matches 8
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Best Local
                                                                                                              YEHY_ECOLI STAN
p3361, P76435,
01-FEB-1994 (Rel.
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
SEQUENCE FROM N
STRAIN=K12 / BH
Richterich P.,
Church G.M.;
                                                                                             YEHY
                                                                                                                                                                                                                                                                                                      Pfam; PF02123; Luteo_ORF3; 1.
PRINTS; PR00914; LVTRUSRNAPOL.
Transferase; RNA-directed RNA;
SEQUENCE 956 AA; 104844 MW;
                                                                                                                                                                                                                                                                                                                                             PIR; B33739; RRBWSC. InterPro; IPR001795;
                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southern bean mosaic virus (SBMV). Viruses; ssRNA positive-strand vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel.
01-MAY-1991 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_
                                                             Bacteria; P
Escherichia
                                                                                                     HYPOTHETICAL ABC
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NCBI_TaxID=12139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P21405;
01-MAY-1991
                                                   NCBI_TaxID=562;
                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                    EMBL; M23021; AAA46565.1;
                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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8; Conser
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      »м N.A.
∕ внв2600;
Р., Lakey
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                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2823471;
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61.5%;
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RNA POLYMERASE (EC 2.7.7.48).
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Last annotation updat
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          Gryan
                                                                       gamma subdivision; Enterobacteriaceae;
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Pred.
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Pred.
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          G.,
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ced. No. 13;
Mismatches
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No.
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           Mintz
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          L.,
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           Robison
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PROP_CAVPO
Q64181;
15-JUL-1999
15-JUL-1999
15-JUL-1999
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TRANSMEM
TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM CONFLICT
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PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U00007; AAA60493.1; ALT_INIT.
EMBL; AE000302; AAC75191.1; -.
EcoGene; EG12011; yehY.
SEQUENCE FROM N.A
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         Cavia porcellus (Guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.!
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
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SIMILARITY: WITH-INTEGRAL MEMBRANE COMPONENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European
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                                                                                                                                                                                                                                                                                                                                                         WGCIGPGCACLQAC 19
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                                                                                                                                                                                                                                                                                                                      WMLVGVGCAWLTAC
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8; Conserv
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                         STANDARD;
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90
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201
245
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343
367
385
                                                    Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                               38.5%;
57.1%;
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E57055E3A2B141CC CRC64;
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                                                    Craniata; Vertebrata; Euteleostomi; Hystricognathi; Caviidae; Cavia.
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01-OCT-1989 (Rel. 12, Last sequence update)
30-MAY-2000 (Rel. 39, Last anotation update)
RESACT RECEPTOR PRECURSOR (GUANYLATE CYCLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYGR_ARBPU P11528;
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                                                                                                                                                                                                    Singh S., Lowe D.G., Thorpe Dangott L.J., Chinkers M., G
                                                                                                                                                                                                                                        TISSUE=Testis;
MEDLINE=88318927; PubMed=2901039;
                                                                                                                                                                                                                                                                                                                                                                  Arbacia punctulata (Punctuate sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                          Echinoidea; Euechinoidea; NCBI_TaxID=7641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                         Nature 334:708-712(1988).
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
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                                                                                                                                                              "Membrane guanylate cyclase to protein kinases.";
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                AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. CATALYTIC ACTIVITY: GTP = 3, '5'-CYCLIC GMP + 1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: SOME SIMILARITY WITH CONSERVED REC
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European Bioinformatics Institute
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                                                                                                   FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON FOR 'RESACT' A CHEMOTACTIC PEPTIDE, AND ON VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENZYME COMPLEXES
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7; Conserv
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Pred. No.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                      SEQUENCE.
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TYPE-1 4.
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                                                                                                                                                                                                                                                                                                                                                   Arbacoida;
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Best Local
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
SPERACT RECEPTOR PRECURSOR (GUNYLAYTE CYCLASE) (EC 4.6.1.2).
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
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              the
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                                                                                                                                                                                     J. Biol.
                                                                                                                                                                                                    the
                                                                                                                                                                                                               "The
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=89197965; PubMed=2564849;
Thorpe D.S., Garbers D.L.;
                                                                                                                                                                                                                                                                              Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                    P16065;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                             STRPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                       This SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                         e membrane form of guanylate cyclase. Homology with a subunit of cytoplasmic form of the enzyme.";

Biol. Chem. 264:6545-6549(1989).

FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON SPERMATOZOA FOR 'SPERACT' A CHEMOTACTIC PEPTIDE, AND ON VARIOUS OTHER CELLS AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE.

CATALYTIC ACTIVITY: GTP = 3.5'. 'CYCLIAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBJECTLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
by non-profit institute.
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                                                                               SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVIGPGCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro; IPR001828; -. PF01094; ANF_receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X12874; CAA31367.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 77. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  986
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508
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568
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361
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                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                               BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          986
507
528
986
836
185
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77.8%;
                                                                              ТО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                                              ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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N-LINKED (GLCNA)
N-LINKED (GLCNA)
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Pred. No.
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                        yright. It is produced through of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESACT RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .) (PO
LINKED (GLCNAC. . .) (PO
LINKED (GLCNAC. . .) (PO
B40238A74CCAFC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
 long

    Phosphorylation;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
          There are
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) (POTENTIAL).
                restrictions
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                            a collaboration
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                           outstation
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RESULT 14
MT2A_RABIT
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Best Local
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                                                                                                                                                                                                                                                                      P18055;
01-NOV-1990 (Rel. 1
01-NOV-1990 (Rel. 2
01-NOV-1997 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                  "Sequence-specific 1H-NMR assignments metallothionein-2.";
                                                                                                                                                                                                                                                        Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    Wagner G., N
Wuetrich K.;
                                                        STRUCTURE BY NMR, MEDLINE=86220204;
                                                                                    Biochem.
                                                                                                        Hunziker P.E., Kaur
                                                                                                                  MEDLINE=95169065; PubMed=7864820;
                                                                                                                           STRAIN-NEW ZEALAND WHITE; TISSUE-Liver,
                                                                                                                                                                  Hunziker P.E.;
"Amino acid se
                                                                                                                                                                                     MEDLINE=92140112;
                                                                                                                                                                                                STRAIN-NEW
                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                   METALLOTHIONEIN-IIA (MT-2A
                                                                                                                                                                                                                                                                                                                   MT2A_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01094; ANF_receptor; Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M22444; AAA30051.1; -.
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
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                                                                                                "Primary
                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                             GCIGPGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q02846; 1AWL
                                                                                                                                                        Enzymol.
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                     structures
J. 306:265-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00452; GUANYLATE_CYCLASES_1; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000719; -.; IPR001054; -.; IPR001828; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                ZEALAND
                                                                                    E., Kaur P., Wan M., Kaenzig A.; ructures of seven metallothioneins 306:265-270(1995).
                                                                                                                                                         sequence determination.";
>1. 205:421-426(1991).
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                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                            , AND SEQUENCE.
; PubMed=3709538;
us D., Worgotter
          157:275-289(1986)
                                                                                                                                                                                    D WHITE; TISSUE=Liver, PubMed=1779803;
                                                                                                                                                                                                                                                                          16, Created)
16, Last sequence update)
35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
1125
510
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1125
839
185
409
                                                                                                                                                                                                                                    us (Rabbit).
Chordata; Craniata; Vertebrata; Euteleostomi;
Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                   37.7%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          126256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPERACT RECEPTOR.
EXTRACELLULAR (POTENT POTENTIAL.
CYTOPLASMIC (POTENTIA PROTEIN KINASE LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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                                              Vasak M.,
                                                                                                                                                                                                                                                                                                                   62
                           in
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29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Lyase;
                                                                                                                            and
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                                                                                                                            Kidney;
                                                                                                                                                                                              Kidney
                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                              Kaegi J.H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1125
                                                                                              rabbit tissue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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RESULT 15
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METAL
                                                                                                        SEQUENCE
                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        helix secondary structure in rabbit liver metallothionein-2.
                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                             Metal-binding; Metal-thiolate cluster;
Cadmium; Acetylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                            PRINTS; PR00860; MTVERTEBRATE.
PROSITE; PS00203; METALLOTHIONEIN_VRT;
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arseniev A., Schultze P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88332998; PubMed=3418714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wuetrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagner G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR.
MEDLINE=86171767; PubMed=3959079;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Three-dimensional structure of rabbit liver [Cd7]metallothionein-2a in aqueous solution determined by nuclear magnetic resonance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaegi J.H.R., Wuetrich K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear magnetic resonance identification of 'half-turn' and 3(10)-
                                37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol.
                                                œ
                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MONOMER.

DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:

DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:

FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA

DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLARE BRIDGES TO 11

CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE

BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.

SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO1. Biol. 201:637-657(1988).
FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE
                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUCOCORTICOIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
                                CCPPGCAKCAQGCI
                                                CIGPGCA-CLQACL
                                                                                                                                                                                                                                                                                                                                                                    2MRB; 15-JUL-92.
                                                                                                                                                                                                                                                                                                                                             PF00131;
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                     IPR003019; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuhaus
                                                                Conservative
                                                                                                                        metalthio;
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                                50
                                               20
                                                                                                                37.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worgotter E.,
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CLUSTER
                                                                       Score 45.5;
Pred. No. 3
                                                                                                      C3FEA7B701081B3E CRC64;
                                                                                                                                                                                                                                                                              CLUSTER
                                                                                                                                                                                                                                                                                                    ACETYLATION.
                                                                Mismatches
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                                                                                                                       Vasak M.,

    Chelation;

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                                                                               DB 1; Length 62;
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                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaegi J.H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagner G., Vasak M.,
                                                                                                                                                                                                                                                                                                                     Zinc;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF CYSTEINE
                                                                                                                                                                                                                                                                                                                   Copper;
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В
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P80290;
01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
01-NOV-1997 (Rel. 2
                                                                                                                                                                                             DOMAIN
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
METALLOTHIONEIN-IIC (MT-2C).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                   METAL
                                                                                                                                                                                                                                                                                        PROSITE; PS00203; METALLOTHIONEIN_VRT; Metal-binding; Metal-thiolate cluster;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR000006; -.
InterPro; IPR003019; -.
                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
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                                                                                                                                                                                                                                                                                 Cadmium;
                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                  Pfam; PF00131; metalthio;
                                                                                                                                                                                                                                                                                                                                           HSSP; P18055; 1MRB
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunziker P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95169065; PubMed=7864820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                        Local
37
                 8
                                                                                                                                                                                                                                                                                                                                                 DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGE TO 11 CYSTEINE LIGANDS. CLUSTER B. THE CORRESPONDING REGION WITHIN THE BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES. SIMILARITY: BELONGS TO FAMILY, 1 IN METALLOTHIONEIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARI TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                            GLUCOCORTICOIDS
CCPPGCAKCAQGCI
                 CIGPGCA-CLQACL
                                 Similarity 57.
8; Conservative
                                                                                                                                                                                                                                                                                                        PR00860; MTVERTEBRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                           P.E., Kaur P., Wan M., Kaenzig A.; structures of seven metallothioneins from J. 306:265-270(1995).
                                                                                                                                                                                                                                                                                 Acetylation.
                                                                          62
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                                 Score 45.5; D
Pred. No. 3.3;
1; Mismatches
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CLUSTER
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BETA.
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                                                                                                                                                                                                                                                                                        1.
Chelation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Kidney;
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                                                  DB 1;
                                  4;
                                                Length 62;
                                  Indels
                                                                                                                                                                                                                                                                                         Zinc; Copper;
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                                  ۲,
                                 Gaps
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Job time: 97 sec

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Minimum
Maximum
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Maximum Match 10
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                            sp_bacteria:*
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                                                                 sp_phage:*
                                                                              sp_organelle:*
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                                                                                                         sp_mammal:*
                                                                                                                   sp_invertebrate:*
          sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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                                                                                                                                   human:*
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. printed

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	₽B	Ħ	Description
, ,	51	41.8	148	2	Q9KN81	Q9kn81 vibrio čhol
2	50	41.0	73	σ	062554	O62554 mytilus edu
ω	50	41.0	73	5	062555	
4.	50	41.0	73	5	Q9U569	₩.
5	50	41.0	73	σ	Q9U568	Q9u568 perna virid
0	50	41.0	75	ψ	096388	096388 perna virid
7	50	41.0	659	ᆫ	028894	O28894 archaeoglob
8	50	41.0	709	ω	Q9P3D2	Q9p3d2 neurospora
9	49	40.2	351	14	Q9E1H5	Q9e1h5 meleagrid h
10	49	40.2	351	14	Q9DPR9	Q9dpr9 meleagrid h
11	49	40.2	1063	13	Q9PWG1	Q9pwg1 oryzias lat
12	48	39.3	67	N	Q9JXZ4	Q9jxz4 neisseria m
13	48	39.3	71	N	Q9JVX6	Q9jv≵6 neisseria m
14	47.5	38.9	161	14	266618	Q66618.equine herp
15	46.5	38.1	315	Ç,	Q93532	Q93532 caenorhabdi
16	46	37.7	230	10	Q9LKQ2	Q91kq2 arabidopsis
17	46	37.7	231	10	Q9FNH6	Q9fnh6 arabidopsis
18	46	37.7	411	w	074310	074310 schizosacch
19	46	37.7	673	ω	013650	013650 schizosacch

Query Match Best Local S Matches 8

Similarity 61.88; Conservative

2;

2; ω --

Length 148; Indels

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Gaps

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444 544 5	39 40 41	3654	321	25 27 28 29	20 21 22 23
44 44 43.5	44 4 44 44 44 44	44.5	444.55555	. 4 4 4 4 0 0 0 0 0 0	45.5 45.5 45.5 45.5
36.1 36.1 36.1 35.7	36.1			3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	37.7 37.7 37.3 37.3
449 790 1055 113	2824 128 348 433	180 214 831	59 59 75 107	175 248 398 1136 47	1125 1127 62 387 731
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Q9NKA5 Q9LQ24 Q9YGW3 Q82765	Q9W7R3 Q44567 Q9VVW4 Q9SYC4	030080 030725 017516	Q9N9H1 Q9U1N5 Q9NG19	Q9S255 Q43033 Q34939 Q04692 Q9N9H0	Q27669 Q9U8P5 Q9TUI5 Q9KG75 Q9KG75
Q9nka5 drosophila Q91q24 arabidopsis Q9ygw3 oryzias lat Q82765 chlamydomon	Q9w/r3 brachydanio O44567 caenorhabdi O9vvw4 drosophila O9syc4 arabidopsis	O30080 archaeoglob O90725 pyrobaculum O17516 caenorhabdi	Q9n9h1 ruditapes p Q9n9h1 ruditapes d Q9u1n5 crassostrea Q9ng19 crassostrea	streptomyc schizosacc leishmania 2 mus muscu venerupis	Q27669 hemicentrot Q9u8p5 diadema set Q9tu15 canis famil Q9tu55 bacillus ha Q9n8d2 trypanosoma

ALIGNMENTS

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Q9KN81;
                                                                                                                                                                                                                                                                                                                                                         STRAIN=EL TOR NIDYD1 / JUNE 19752301;
MEDLINE=20406833; PubMed=10552301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Wichardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., White O.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., White O.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., White O.,
                                                                                       SMART; SM00422; HTH_MERR; 1.
DNA-binding; Transcription regulation.
SEQUENCE 148 AA; 16986 MW; 6987166A8CD35508 CRC64;
                                                                                                                                        InterPro; IPR000551; ...

Pfam; PF00376; merr; 1.

PRINTS; PR00040; HTHMERR.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                             EMBL; AE004351; AAF95998.1;
TIGR; VCA0084; -.
                                                                                                                                                                                                                                                                                                      cholerae.
                                                                                                                                                                                                                                                                                                                                     Ermolaeva M.D., Vamathevan J., Bass S., Qin
McDonald L., Utterback T., Fleishmann R.D.,
Salzberg S.L., Smith H.O., Colwell R.R., Mei
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                     DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                  41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Vibrionaceae; Vibrio.
Score 51; DB Pred. No. 3.5; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                DB
3.5;
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Best Local
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Best Local
                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                062555 PRELIMINARY;
062555;
01-AUG-1998 (Tremblrel. 07, C1
01-AUG-1998 (Tremblrel. 15, L2
01-OCT-2000 (Tremblrel. 15, L2
METALLOTHONEIN 10 II.
                                                                                                                                              PRINTS; | PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                         Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca;
Mytiloidea; Mytilidae; Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barsyte D., White K.N., Love Submitted (APR-1998) to the EMBL; AJ005453; CAA06550.1;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=DIGESTIVE GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (Tremblrel. 07, 01-OCT-2000 (Tremblrel. 15, METALLOTHIONEIN 10 TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00131; metalthio; 1.
PRINTS; PR00875; MTMOLLUSC.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
SEQUENCE 73 AA; 7220 MW; 76797FB0FCD7B3B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=DIGESTIVE GLAND;
Barsyte D., White K.N., Love
Submitted (APR-1998) to the
EMBL; AJ005452; CAA06549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O62554;
01-AUG-1998 (TrEMBLrel.
                                                                                                                                                                                      InterPro; IPR003019; -.
Pfam; PF00131; metalthio;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000561; -.
InterPro; IPR001008; -.
InterPro; IPR003019; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6550;
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                         Similarity
8; Conserv
                                                                                                                       F00131; metalthio; 1.
PR00875; MTMOLLUSC.
; PS00022; EGF 1; UNKNOWN 1.
E 73 AA; 7153 MW; 20CFA4CB3A0CDE19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                         41.0%;
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                                                                                                                                                                                                                                                                                                         Lovejoy
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Pred. No.
                                         Score 50; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                Bivalvia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                       Mismatches
                                                                                                                                                                                                                                                                                                         D.A.;
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2.7;
                                           DB
2.7;
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                                                          Length 73;
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Q9U568
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Interpro; IPRO03019; -.
Interpro; IPRO03019; -.
Prims; PRO0131; metalthio; 1.
PRINTS; PRO0875; MYMOLLUSC.
R PROSITE; PS00022; EGF_1; UNKNOWN_1.
R PROSITE; PS00022; EGF_1; UNKNOWN_1.
  Query Match
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Best Local
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                                                      green mussel, Perna viridis.";
JEXP. 2001. 284:445-453(1999).
EMBL; AF092972; AAF22487.1;
InterPro; IPR000561;
InterPro; IPR001008;
InterPro; IPR003019;
InterPro; IPR003019;
Pfam; PF00131; metalthio; 1.
PRINTS; PR00875; MIMOLLUSC.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
SEQUENCE 73 AA; 7277 MW; ABCEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   green mussel, Perna viridis.";
J. Exp. Zool. 284:445-453(1999).
EMBL; AF092971; AAF22486.1;
InterPro; IPR000561;
InterPro; IPR001008;
InterPro; IPR001008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9U568;
Q9U568;
01-MAY-2000
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Q9U569;
Q1-MAY-2000
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=99379847; PubMed=10451422;
Khoo H.W., Patel K.H.;

"Metallothionein cDNA, promoter, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Mytiloidea; Mytilidae; Perna. NCBI_TaxID=73031;
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mo
Mytiloidea; Mytilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                Perna viridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 METALLOTHIONEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khoo H.W., Patel K.H.;
"Metallothionein cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=73031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99379847; PubMed-10451422;
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8; Conserv
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) (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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  41.0%;
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MW; ABCEAD9547DF5CA7
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Best Local S
Matches
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"Green mussel (Perna viridis) metallothionein cDNA.";

L Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF036904; AAD02054.1; -.

R InterPro; IPR000561; -.

R InterPro; IPR001008; -.

R InterPro; IPR003019; -.

R InterPro; IPR003019; -.

R InterPro; IPR003019; -.

R Pfam; PF00131; metalthio; 1.

R Pfam; PF00131; metalthio; 1.
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       Klenk H.-P., Clayton R.A., Tomb J.-F., white O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Peterson S., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbek R., Gocayne J.D., Weldman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Sadow P.W., Olsen G.J., Fraser C.M., Smith H.O., Hoese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O28894;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096388;
01-MAY-1999
                                                                                                                                                                                                                                                     STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
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Mytiloidea; Mytilidae; Perna.
MCBI_TaxID=73031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perna viridis.
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CEMBLrel. 05,
CEMBLrel. 16,
REDUCTASE, S
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Bowman C., ruj-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update), Last annotation update) SUBUNIT A (HDRA-2).
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01-MAR-2001
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Q9P3D2;
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SEQUENCE
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PROSITE; PS00198; 4FE4S_FEXEDOXIN; 3.
PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
Hypothetical protein; Iron-sulfur.
Hypothetical protein; Iron-sulfur.
SEQUENCE 659 AA; 72068 MW; 4D624A0AFAC01812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.;
"The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390.364-370(1997).
EMBL; AE001009; AAB89867.1; -.
HSSP; P00198; 1FCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schulte U., Aign V., Nyakatura G., Mewes |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariales; Sordariaceae; Neurospora.
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
RELATED TO LONG-CHAIN-FATTY-ACID--COA LIGASE FAA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000205; -.
InterPro; IPR001450; -.
InterPro; IPR001467; -.
Pfam; PF00037; fer4; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR0008
PROSITE; PS00455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2000) to the EMBL; AL390189; CAB99181.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora
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11; Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                       Score 50;
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Viruses; dsDNA viruses, n
Gammaherpesvirinae.
NCBL_TaxID=37108;
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Kingham B.J., Zelnik v., Aver--
Schmidt C.J.;
Schmidt C.J.;
"Coding potential of herpesvirus of turkey: comparative g.
"Coding potential of herpesvirus of turkey: comparative g.
analysis of Marek's disease serologically related viruses
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282130; AAG30055.1; -.
EMBL; AF282130; AAG30055.1; -.
EMBL; AF282130; AAG30055.1; -.
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Meleagrid herpesvirus 1
Viruses; dsDNA viruses, 1
Gammaherpesvirinae.
NCBI_TaxID=37108;
[1]
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Q9PWG1;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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01-MAR-2001
UL16 TEGUMEN
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"The genome of turkey herpesvirus.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AF291866; AAG45753.1; -.
SEQUENCE 351 AA; 39137 MW; FDB1745E4ADA71:
                         OLGC2.

Oryzlas latipes (Medaka fish).

Oryzlas latipes (Medaka fish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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no RNA stage; Herpesviridae;
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; Herpesviridae;
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"Oryzias latipes mRNA for membrane guan)
Submitted (JUL-1999) to the EMBL/GenBani
EMBL; AB030274; BAA82623.1; -.

HSSP; Q02846; 1AWL.
InterPro; IPR001054; -.
InterPro; IPR001170; -.
InterPro; IPR001170; -.
InterPro; IPR0011245; -.
InterPro; IPR001245; -.
InterPro; IPR001024; ANF_receptor; 1.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF001094; ANF_receptor; 1.
Pfam; PF001094; ANF_receptor; 1.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00452; GUANYLATE_CYCLASES; 1
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HYPOTHETICAL !
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SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; pubMed=10710307;
MEDLINE-20175755; pubMed=10710307;
MEDLINE-2017575; pubMed=10710307;
MEDLINE-2017575; pubMed=10710307;
MEDLINE-20175755; pubMed=107107; pubMed=107107; pubMed=107107; pub
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Q9JXZ4;
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SEQUENCE
                                                                                                                                                                                                                           Science 287:1809-1815(2000)
EMBL; AE002532; AAF42160.1;
TIGR; NMB1825; -
                                                                                                                                                                 Hypothetical SEQUENCE 6
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Bacteria; Proteobacteria; beta subdivisi
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1063 AA;
                                                                                                                                                                 al protein.
67 AA; 7569 MW;
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                                  48;
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37;
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Matches 9
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01-NOV-1996
01-NOV-1996
01-MAR-2001
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                Telford E.A.R.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20824; AAC13801.1; -.
SEQUENCE 161 AA; 17750 MW; C49163D3E254F773 CRC64;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLLNB=95302501; PubMed=7783207;

Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;

"The DNA sequence of equine herpesvirus 2.";

J. Mol. Biol. 249:520-528(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, Gammaherpesvirinae.
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MEDLINE=20222556; PubMed=10761919;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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27 ESWECCGSDCGDACIQ 42
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Q93532;
Q1-FEB-1997
Q1-FEB-1997
Q1-MAR-2001
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Bonfield J., Burton J., Connell M., Copsey T., Coulson A
Craxton M., Dear S., Du Z., Dunkin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roppra A.,
Parsons J., Percy C., Rifken E., Roppra A.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                      InterPro; IPR001507
SMART; SM00241; ZP;
SEQUENCE 315 AA;
                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
EMBL; 278542; CAB01742.1; -.
InterPro; IPR001507; -.
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Rhabditidae; Peloder
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                                                                                                                             2;
                                                                                                                                                               Score 46.5;
Pred. No. 30;
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                                                                                                                                 Mismatches
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Maximum Match 100%
Listing first 45 summaries
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A.Geneseq_0601:*
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2: /SIDS8/gcgdata/
3: /SIDS8/gcgdata/
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122
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Copyright (c) 1993 - 2000 Com
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ErbB2 binding pept	ErbB2 binding pept	ErbB2 binding pept	ErbB2 binding pept	HER2 peptide ligan	Amino acid sequenc	HER2 peptide ligan	HER2 peptide ligan	HER2 peptide ligan	Amino acid sequenc	ErbB2 binding pept	Description		

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binding pep binding pep	ErbB2 binding pept

ALIGNMENTS

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RESULT
AAB76363
                                                                                            10-APR-2001 (first entry)
                                                                                     ErbB2 binding peptide amino acid sequence SEQ ID 14.
                                                                                                          AAB76363 standard; Peptide;
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Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's Chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.

Synthetic.

WO200101748-A2

11-JAN-2001.

30-JUN-2000; 2000WO-US18283

02-JUL-1999; 99US-0142232

(GETH) GENENTECH INC

WPI; 2001-123048/13.

Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy - $\frac{1}{2} \left(\frac{1}{2} \right) = \frac{1}{2} \left(\frac{1}{2} \right) \left(\frac{1}{$

Disclosure; Figure

16;

116pp; English

invention

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non-naturally occurring

peptide ligands known as HER2).

Peptides

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Matches 20
bind to the human erbB2 gene product ErbB2 (also known as H represented in AAB76350 - AAB76420 and AAB76430 - AAB76509 of the ErbB2 binding ligands of the invention. Sequences AAB76421 - AAB76431 represent antibodu po emino erica erica expensions.
                                                                                                                                                                                                                                                                    Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -  \frac{1}{2} \frac{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolic disorder;
Parkinson's disease
Down's syndrome; ne
                                                                                                                                                                                                            Disclosure; Figure 8A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; nervous system disease; stroke; ischaemia; nutritional deficiency; Alzheimer's disease; epilepsy, multiple sclerosis; Huntington's chorea; rve deafness; Meniere's disease; diabetic neuropathy.
      represent antibody Fc amino acid sequences
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Pred. No. 7.1e-09;
Mismatches 0;
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                                                              e ligands which
s HER2). Peptide
09 are examples
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Query Match Best Local Matches

Similarity

100.0%; clarity 100.0%; Conservative (

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Score 122; I Pred. No. 1e-); Mismatches

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Length Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.
                                      The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a particul
                                                                                                                                                                                  Novel fusion polypeptides comprising a functions to target hybrid molecule to constant region multimerization domain
                                                                                                                                                                                                                                             WPI; 2001-123106/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HER2 peptide ligand #4
Sequence
                            target molecule.
                                                                                                                                                                                                                                                                                                                                  02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin; multidimerization domain; ligand
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Pred. No. 7.1e-09;
; Mismatches 0;
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                                                                                                                                                                                                 peptide ligand domain which target cell, and immunoglob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a fusion protein, comprising peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising
                                           Fusion protein; immunoglobulin; multidimerization domain; ligand.
                                                                                               HER2 peptide ligand
                                                                                                                                                                                                 AAB67214;
                                                                                                                                                                                                                                                AAB67214 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target molecule.
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Pred. No. 1.3e-08;
; Mismatches 0;
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                                                                                                                                                                                                      Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain .
                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                            10-APR-2001
                                                                                                                                                                                                                                                                                                                      AAB76431 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                             02-JUL-1999;
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                                                                                                                          11-JAN-2001.
                                                                                                                                                WO200101748-A2
                                                                                                                                                                                             Down's
                                                                                                                                                                                                                                                   Amino acid sequence of (1.1FI)2-Z SEQ ID 82.
                                                                                                                                                                                                                                                                                                  AAB76431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target molecule.
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                                                      (GETH )
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                                                                                                                                                                                           syndrome; nerve
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                              9905-0142232
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                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                             deafness; Meniere's disease;
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Pred. No. 1.4e-08;
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WPI; 2001-123048/13

Dennis MS

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC This invention relates to non-naturally occurring peptide ligands which CC bind to the human erbb2 gene product ErbB2 (also known as HER2). Peptides CC represented in AAB76350 - AAB76421 and AAB76432 - AAB764509 are examples CC of the ErbB2 binding ligands of the invention. Sequences used in CC the isolation of the peptides of the invention. The peptides compete for CC binding ErbB2 with naturally occurring ligands, and may be used to treat CC disorders characterized by over expression of HER2/ErbB2 such as cancers, CC diseases of the nervous system, musculature and epithelia, e.g. nervous CC system damage resulting from trauma, surgery, strokes, ischaemia, CC infection, metabolic disorders, nutritional deficiency or toxic agents. CC infection, metabolic disorders, nutritional deficiency or toxic agents. CC infection data the synthetic peptide ligands may be used to treat CC In particular the synthetic peptide ligands may be used to treat CC lifemer's disease, Parkinson's disease, epilepsy, multiple sclerosis, CC Huntington's Chorea, Down's syndrome, nerve deafness, Meniere's disease conductors.
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Best Local :
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                  the
                            The present invention relates to a fusion protein, comprising peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (ID). The hybrid molecules comprising
                                                                                                                                                                                                                                  Dennis MS,
                                                                                                                                                                                                                                                                                                   02-JUL-1999;
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   ij
                                                                                                Example 1;
                                                                                                                               Novel fusion polypeptides comprising a functions to target hybrid molecule to constant region multimerization domain
                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000WO-US18185
                                                                                                                                                                                                                                                                                                                                                                                                WO200102440-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HER2 peptide ligand
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                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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stide ligands and their functional derivatives can be us same applications as, a peptide ligand can be used. For
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                                                                                                                                                                                                                                 Lazarus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin; multidimerization domain; ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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Pred. No. 1.4e-08;
Mismatches 0;
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                                                                                                                                            peptide ligand domain which target cell, and immunoglob
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                                                                                                                                               immunoglobulin
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                                                                                                                                     This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences used in AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HEB2/ErbB2 such as cancers,
                                           In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease
                                                                                       diseases of the nervous system, musculature and epithelia, e.g. system damage resulting from trauma, surgery, strokes, ischaemia infection, metabolic disorders, nutritional deficiency or toxic
                                                                                                                                                                                                                                                                                                                       Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Sequence
                                                                                                                                                                                                                                                                                     Disclosure; Figure 16;
                                                                                                                                                                                                                                                                                                                  multiple scierosis and diabetic neuropathy
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                                                                                                                                                                                                                                                                                                                                                                                                                Dennis MS
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                                with diabetes.
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Query Match

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                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences used in AAB76421 - AAB76631 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                   In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
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                                                                                                                                                   Score 94; DB 22; Pred. No. 1.8e-05;
                                                                                                                         Mismatches
                                                                                                                                                                             Length 17;
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                                                                    AAB76365;
                                                                                                                 AAB76365
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                                                                                                                 Peptide;
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Synthetic
                         metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy
                                                                                                       ErbB2 binding peptide amino
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                            erbB2; HER2;
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                                                                            cancer;
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                                                                                                       sequence SEQ ID
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                                                                          system disease; stroke;
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RESULT
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Matches
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02-JUL-1999;
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les 13; Conservative
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99US-0142232
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
                                                                                                                                                                                                                           02-JUL-1999;
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Non-naturally occurring peptide ligands which compete for binding human
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Pred. No. 0.00011;
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This invention relates to non-naturally occurring peptide ligands which CC bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides crepresented in AAB76350 - AAB76420 and AAB76422 - AAB76509 are examples CC of the ErbB2 binding ligands of the invention. Sequences used in CC the isolation of the peptides of the invention. The peptides compete for CC binding ErbB2 with naturally occurring ligands, and may be used to treat CC disorders characterized by over expression of HER2/ErbB2 such as cancers, CC diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, CC infection, metabolic disorders, nutritional deficiency or toxic agents. CC infection, metabolic disorders, nutritional deficiency or toxic agents. CC In particular the synthetic peptide ligands may be used to treat CA lzheimer's disease, Parkinson's disease, pultiple sclerosis, CC Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease can not the contract of the contract 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erB2 gene products, useful for treating e.g. multiple sclerosis and diabetic neuropathy - \,
Sequence
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AAB76360
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Best Local Similarity
Matches 13; Conserv 10-APR-2001 AAB76360; AAB76360 standard; \vdash 4 ESWGCIGPGCACLQACL 20 eewgcigpgcaclinci Conservative (first entry) Peptide; 71.3%; 76.5%; 17 Score 87; DB. Pred. No. 0.00 l; Mismatches 20 DB 22; 0.00013; Length 17 Indels 0 Gaps 0

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В

Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy

ErbB2 binding

peptide amino acid sequence

SEQ

IJ

11

WO200101748-A2

11-JAN-2001

30-JUN-2000; 2000WO-US18283

02-JUL-1999; 99US-0142232

(GETH) GENENTECH INC

PTT

Dennis

WPI; 2001-123048/13

Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -

Disclosure; Figure 16; 116pp; English.

This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptide represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples

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Best Local Similarity 81.2%;
Matches 13; Conservative
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Maximum DB seq length: 200000000
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   is derived by analysis of the total score distribution
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Packfiles1.pep:*
                                US-08-417-495-26
US-08-284-991B-26
US-09-218-950-26
US-09-218-950-26
PCT-US92-01785-26
PCT-US92-01785-26
PCT-US95-00454-26
US-09-413-814-20
US-08-751-205-3
US-08-795-445A-53
US-08-795-447A-53
US-08-795-446B-53
US-08-795-446B-53
US-08-462-108-1
US-08-467-98-38-4
US-08-464-38-6
US-08-464-38-6
US-08-464-38-6
US-08-468-545B-6
US-08-468-545B-6
US-08-468-545B-6
US-08-468-545B-6
US-08-356-786-2
US-08-466-318A-12
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22.823 Million cell updates/sec
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Sequence 26, Appl
Sequence 26, Appl
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Sequence 20, Appl
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Sequence 30, Appl
Sequence 31, Appl
Sequence 53, Appl
Sequence 64, Appl
Sequence 4, Appl
Sequence 68, Appl
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42	42	42	42	42	42	42.5	42.5	43	43.5	43.5	43.5	43.5	44	44	44.5	44.5	44.5
34.4	34.4	34.4	34.4	34.4	34.4	34.8	34.8	35.2	35.7	35.7	35.7	35.7	36.1	36.1	36.5	36.5	36.5
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Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	6	47,	Sequence 7, Appli	7,	Sequence 3, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 68, Appl		Sequence 189, App	Sequence 30, Appl	Sequence 12, Appl	Sequence 30, Appl

ALIGNMENTS

Chimeras

RESULT 1 US-08-417-495-26

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Sequence 26, Application US/08417495
Patent No. 5843728
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
                                                                                                                                                                                                    APPLICATION NUMBER: US/07/847,566
FILING DATE:
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/COURT NUMBER: 00.786/11900
                                                                  TELEFAX: (617) 542-8900
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TYPE: amino acids
TOPOLOGY: line
WOLECUT
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                            REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: IBM P.C. DOS (Version SOFTWARE: Wordperfect (Version 5.0) CURRENT APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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 amino acids
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RESULT 3
US-09-218-950-26
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US-08-284-391B-26
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Best Local
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MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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                                                                                                                                                                                       Local Similarity nes 7; Conservat
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nes 7; Conserv
                                                                                           15 LFLSYACLGPGCQALR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 02-AUG-1994
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                                                                                                                                           2 VYESWGCIGPGCACLQ 17
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Romeo, Charles
Kolanus, Waldemar
VENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                    Length 220;
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                                                                                                                                                                                                              PCT-US92-01785-26
                                                                                                                                                                                                                                         RESULT
                                                                   Sequence 26, Application PC/TUS9201785
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor
TITLE OF INVENTION: Chimeras
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 620%...
Patent No. 62
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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APPLICANT:
APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
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MEDIUM TYPE: Disketi
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 07/6/
APPLICATION NUMBER: 07/6/
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APPLICATION NUMBER: 07/8/
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APPLICATION NUMBER: 07/8/
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               15 LFLSYACLGPGCQALR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Elbing, Karen L REGISTRATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/218,950
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                                                                                                                                                                                                                                                                                                                                                         2 VYESWGCIGPGCACLQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26, Application US/09218950
o. 6284240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617-428-7045
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Banapour, Babak
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Pred. No.
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17;
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/665,961
FILING DATE: MATCH 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/119002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01785
FILING DATE: 19920306
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                             COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM PS.C DOS (Version 3.30)
SOPTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/665,961
                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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LENGTH: 220 amino acid
                                     CLASSIFICATION:
                                                    APPLICATION NUMBER: 0: FILING DATE: March 6,
                                                                                                                             FILING DATE:
                                                                                                                                              APPLICATION NUMBER: PCT/US95/00454
                                                                                                                                                                                                                                                                           ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & NATIONAL STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LFLSYACLGPGCQALR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VYESWGCIGPGCACLQ 17
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02110-2804
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43.8%;
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                                                                        07/847,566
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RESULT 7
US-08-751-305-33
; Sequence 33, Application US/08751305
; Patent No. 5965439
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; MOLECULE TYPE:
PCT-US95-00454-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofie, Gerhard
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 20
LENGTH: 243
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                       Query Match 40.2%;
Best Local Similarity 42.1%;
Matches 8; Conservative
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Patent No. 622506
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                            83 RVSVAWACLGMIRACLETC 101
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REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LFLSYACLGPGCQALR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: March 7, 1991
                                                                                                                                                1 QVYESWGCIGPGCACLQAC 19 : | : | |: | ||: |
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43.8%;
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                                                                                                                                                                                                       Mismatches
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GENERAL INFORMATION:

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Query Match
Best Local Similarity
"hes 9; Conserv
                                                                                                                          ; ORGANISM: Human US-09-368-590-2
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; MOLECULE TYPE:
US-08-751-305-33
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-368-590-2
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                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 \,
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Solimena, Michele
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09368590 Patent No. 6187563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                            TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR TITLE OF INVENTION: AUTOANTICENS OF AUTOIMMUNE DISEASES FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/751, FILING DATE: 18-NOV-1996 CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION: NAME: Wetherell, Jr., John R. REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                            TYPE: PRT
                                                                                                                                                                         LENGTH: 2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07306/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tenner et al., Andrea J. TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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TTTY: La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
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QVYESWGCIGPGCA 14
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amino acid
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                                                 39.3%;
64.3%;
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                                                 Score 48; DB 4;
Pred. No. 2.4e+02;
                                  Mismatches
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                                                                 Length 2293;
                                  Indels
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                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                       Sequence 53, Application US/08795445A
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Best Local
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STREET: 1540 CITY: Thousand Oaks
STATE: California
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
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                                                                               CORRESPONDENCE ADDRESS:
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                                                                                            TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                        46 GCCGGGTACACCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/974,022 FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                              ADDRESSEE:
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o. 6015938
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                                              E: Amgen Inc.
1840 Dehavilland Drive
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Lacey, David L.
Calzone, Frank J.
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-795-445A-53
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Patent No. 6284728
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/795,447A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 9; Conserv
                                                                                                                                                  FILING DATE: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                           CITY: Thousand Oaks
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                            STRANDEDNESS:
                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                          ENGTH:
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                                       amino acids
                                                                                                                                                                                                                                                                                                                        California
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One Amgen Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lacey, David L.
Calzone, Frank J.
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linear
            linear
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RESULT 13
US-08-795-446B-53
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Best Local Similarity
"hes 9; Conserv?
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                                                                            ; Patent No. 6288032
; GENERAL INFORMATION:
                                                                                     Sequence 53, App...
Sequence 53, App...
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 102 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
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CLASSIFICATION:
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STATE: California
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9; Conserva
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                                                                                                          Application US/08795446B
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Pred. No.
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CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES:

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US-08-422-108-1
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Best Local Similarity
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3:
FILING DATE: 13-DEC-1994
PRIOR APPLICATION DATA:
                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
FILING DATE: 14-App-1995
CLASSIFICATION: 435
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                  COUNTRY: UZIP: 94080
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TOPOLOGY: li
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CITY: Thousand Oaks
                                                                                                                                       SOFTWARE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                    Shepard,
Ullrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1840 Dehavilland Drive
                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                    WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                    Hudziak,
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                                                                                                                                                                                                                                                                                        Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.7%;
                                                                                                                                                                                                                                                                                                                                                                                     Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                      H. Michael
                                              08/355460
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08/048346
                                                                                                                                                                                                                                                                                           Inc.
                                                                                                                                                                                  1.44 Mb floppy disk
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Best Local Similarity
'--+ches 7; Conserva
US-09-146-283-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-146-283-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-422-108-1
                                                                                                                 TELEFAX: 650-324 ... 1NFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: 1-FNGTH: 782 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application Patent No. 5976546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
                               HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: hom
                                                               TOPULOU.
MOLECULE TYPE: PI
                                                                                                                                                                                                     REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,
                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/146,283
FILING DATE: 03-SEPT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/3:
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wu, Hon TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 CVGEGLACHQLC 494
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lee, Wendy M
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
               ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CIGPGCACLQAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA
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                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dehlinger & Associates
O Cambridge Ave. Suite 250
                                                                                                                                                                                                                                                                                                                        03-SEPT-1998
                                                                               protein
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58.3%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 624;
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Query Match
Query Match
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 8 CIGPGCACLQAC 19
| | | | | | | |
Db 504 CYGEGLACHQLC 515

Search completed: November 21, 2001, 15:45:25
Job time: 28 sec
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